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(54) Primers for synthesising full-length cDNA and their use

(57) Primers for synthesizing full-length cDNAs and their use are provided.

5602 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3' -ends of the cDNA have been determined. Furthermore, primers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

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Description

FIELD OF THE INVENTION

[0001] The present invention relates to a polynucleotide encoding a novel protein, a protein encoded by the polynucleotide, and new uses of these.

BACKGROUND OF THE INVENTION

[0002] Currently, the sequencing projects, the determination and analysis of the genomic DNA of various living organisms have been in progress all over the world. The whole genomic sequences of more than 10 species of prokaryotes, a lower eukaryote, yeast, and a multicellular eukaryote, C. elegans are already determined. As to human genome, which is supposed to be composed of three thousand million base pairs, the world wide cooperative projects have been under way to analyze it, and the whole structure is predicted to be determined by the years 2002-2003. The aim of the determination of genomic sequence is to reveal the functions of all genes and their regulation and to understand living organisms as a network of interactions between genes, proteins, cells or individuals through deducing the information in a genome, which is a blueprint of the highly complicated living organisms. To understand living organisms by utilizing the genomic information from various species is not only important as an academie subject, but also socially significant from the viewpoint of industrial application.

[0003] However, determination of genomic sequences itself cannot identify the functions of all genes. For example, as for yeast, only the function of approximately half of the 6000 genes, which is predicted based on the genomic sequence, was able to be deduced. As for human, the number of the genes is predicted to be approximately one hundred thousand. Therefore, it is desirable to establish "a high throughput analysis system of the gene functions" which allows us to identify rapidly and efficiently the functions of vast amounts of the genes obtained by the genomic sequencing.

[0004] Many genes in the eukaryotic genome are split by introns into multiple exons. Thus, it is difficult to predict correctly the structure of encoded protein solely based on genomic information. In contrast, cDNA, which is produced from mRNA that lacks introns, encodes a protein as a single continuous amino acid sequence and allows us to identify the primary structure of the protein easily. In human cDNA research, to date, more than one million ESTs (Expression Sequence Tags) are publicly available, and the ESTs presumably cover not less than 80% of all human genes.

[0005] The information of ESTs is utilized for analyzing the structure of human genome, or for predicting the exon-regions of genomic sequences or their expression profile. However, many human ESTs have been derived from proximal regions to the 3'-end of cDNA, and information around the 5'-end of mRNA is extremely little. Among these human cDNAs, the number of the corresponding mRNAs whose encoding protein sequences are deduced is approximately 7000, and further, the number of full-length therein is only 5500. Thus, even including cDNA registered as EST, the percentage of human cDNA obtained so far is estimated to be 10-15% of all the genes.

[0006] It is possible to identify the transcription start site of mRNA on the genomic sequence based on the 5'-end sequence of a full-length cDNA, and to analyze factors involved in the stability of mRNA that is contained in the cDNA, or in its regulation of expression at the translation stage. Also, since a full-length cDNA contains ATG, the translation start site, in the 5'-region, it can be translated into a protein in a correct frame. Therefore, it is possible to produce a large amount of the protein encoded by the cDNA or to analyze biological activity of the expressed protein by utilizing an appropriate expression system. Thus, analysis of a full-length cDNA provides valuable information which complements the information from genome sequencing. Also, full-length cDNA clones that can be expressed are extremely valuable in empirical analysis of gene function and in industrial application.

[0007] Therefore, if a novel human full-length cDNA is isolated, it can be used for developing medicines for diseases in which the gene is involved. The protein encoded by the gene can be used as a drug by itself. Thus, it has great significance to obtain a full-length cDNA encoding a novel human protein.

[0008] In particular, human secretory proteins or membrane proteins would be useful by itself as a medicine like tissue plasminogen activator (TPA), or as a target of medicines like membrane receptors. In addition, genes for signal transduction-associated proteins (protein kinases, etc.), glycoprotein-associated proteins, transcription-associated proteins, etc. are genes whose relationships to human diseases have been elucidated. Moreover, genes for disease-associated proteins form a gene group rich in genes whose relationships to human diseases have been elucidated.

[0009] Therefore, it has great significance to isolate novel full-length cDNA clones of human, only few of which has been isolated. Especially, isolation of a novel cDNA clone encoding a secretory protein or membrane protein is desired since the protein itself would be useful as a medicine, and also the clones potentially include a gene associated with diseases. In addition, genes encoding proteins that are associated with signal transduction, glycoprotein, transcription, or diseases are expected to be useful as target molecules for therapy, or as medicines themselves. These genes form a gene group predicted to be strongly associated with diseases. Thus, identification of the full-length cDNA clones

encoding those proteins has great significance.

SUMMARY OF THE INVENTION

[0010] An objective of the present invention is to provide a polynucleotide encoding a novel protein, a protein encoded by said polynucleotide, and novel usages of these.

[0011] The inventors have developed a method for efficiently cloning a human full-length cDNA that is predicted by the ATGpr etc. to be a full-length cDNA clone, from a full-length-enriched cDNA library that is synthesized by the oligo-capping method. Then, the inventors determined the nucleotide sequence of the obtained cDNA clones from both 5'- and 3'- ends.

[0012] Furthermore, the inventors analyzed the obtained clones by the BLAST search of the databases, SwissProt (http://www.ebi.ac.uk/ebi_docsSwissProt_db/swisshome.html), GenBank (http://www.ncbi.nlm.nih.gov/web/GenBank), and UniGene (Human) (http://www.ncbi.nlm.nih.gov/UniGene).

[0013] The full-length cDNA clones of the present invention have high fullness ratio since these were obtained by the combination of (1) construction of a full-length-enriched cDNA library that is synthesized by the oligo-capping method, and (2) a system in which the full-length ratio is evaluated from the nucleotide sequence of the 5'-end (selection based on the ATGpr, previously removed complete sequences to ESTs). However, the primer of the present invention enables to obtain full-length cDNA easily without any specialized methods as in the described method.

Homology analysis in which the analysis is carried out against a not-full-length cDNA fragment to postulate the function of a protein encoded by said fragment, is being commonly performed.

However, since such analysis is based on the information of the fragment, it is not clear as to whether this fragment corresponds to a part that is functionally important in the protein. In other words, the reliability of the homology analysis based on the information of a fragment is doubtful, as information related to the structure of the whole protein is not available. However, the homology analysis of the present invention is conducted based on the information of a full-length cDNA comprising the whole coding region of the cDNA, and therefore, the homology of various portions of the protein can be analyzed. Hence, the reliability of the homology analysis has been dramatically improved in the present invention.

[0014] The inventors completed the invention by finding that it is possible to synthesize a novel full-length cDNA by using the combination of a primer that is designed based on the nucleotide sequence of the 5'-ends of the selected full-length cDNA clones and any of an oligo-dT primer or a 3'-primer that is designed based on the nucleotide sequence of the 3'-ends of the selected clones.

[0015] Thus, the present invention relates to primers described below, a method for synthesizing a polynucleotide using the primers, and polynucleotides obtained by the method.

[0016] First, the present invention relates to

(1) use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides;

(2) a primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides; and

(3) a primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence / 3'-end nucleotide sequence is selected from the combinations of 5'-end nucleotide sequence / 3'-end nucleotide sequence set forth in the SEQ ID NOs in Tables 1 and 2.

[0017] Tables 1 and 2 shows names of clones obtained in the examples described later, comprising the polynucleotide of the present invention (Table 1; 5547 clones, Table 2; 54 clones), names of nucleotide sequences at the 5'-end and 3'-end of the full-length cDNA, and their corresponding SEQ ID NOs. A blank indicates that the 3'-end sequence corresponding to the 5'-end sequence has not been determined for the same clone.

[0018] The SEQ ID NO of a 5'-end sequence is shown on the right side of the name of the 5'-end sequence, and the SEQ ID NO of a 3'-end sequence is shown on the right side of the name of the 3'-end sequence.

Table 1

name of clone	name of 5'-end sequence	SEQ ID of 5'-end sequence	name of 3'-end sequence	SEQ ID of 3'-end sequence
HEMBA1000005	F-HEMBA1000005	1	R-HEMBA1000005	5548
HEMBA1000012	F-HEMBA1000012	2		
HEMBA1000020	F-HEMBA1000020	3		
HEMBA1000030	F-HEMBA1000030	4	R-HEMBA1000030	5549
HEMBA1000042	F-HEMBA1000042	5	R-HEMBA1000042	5550
HEMBA1000046	F-HEMBA1000046	6	R-HEMBA1000046	5551
HEMBA1000050	F-HEMBA1000050	7	R-HEMBA1000050	5552
HEMBA1000076	F-HEMBA1000076	8	R-HEMBA1000076	5553
HEMBA1000111	F-HEMBA1000111	9	R-HEMBA1000111	5554
HEMBA1000129	F-HEMBA1000129	10	R-HEMBA1000129	5555
HEMBA1000141	F-HEMBA1000141	11	R-HEMBA1000141	5556
HEMBA1000150	F-HEMBA1000150	12	R-HEMBA1000150	5557
HEMBA1000156	F-HEMBA1000156	13	R-nnnnnnnnnnnn	5558
HEMBA1000158	F-HEMBA1000158	14	R-HEMBA1000158	5559
HEMBA1000168	F-HEMBA1000168	15	R-nnnnnnnnnnnn	5560

PLACE1004937	F-PLACE1004937	4478	R-PLACE1004937	9454
PLACE1004969	F-PLACE1004969	4479	R-PLACE1004969	9455
PLACE1004972	F-PLACE1004972	4480	R-PLACE1004972	9456
PLACE1004979	F-PLACE1004979	4481	R-PLACE1004979	9457
PLACE1004982	F-PLACE1004982	4482	R-PLACE1004982	9458
PLACE1004985	F-PLACE1004985	4483	R-PLACE1004985	9459
PLACE1005026	F-PLACE1005026	4484	R-PLACE1005026	9460
PLACE1005027	F-PLACE1005027	4485	R-PLACE1005027	9461
PLACE1005046	F-PLACE1005046	4486	R-PLACE1005046	9462
PLACE1005052	F-PLACE1005052	4487	R-PLACE1005052	9463
PLACE1005055	F-PLACE1005055	4488		
PLACE1005066	F-PLACE1005066	4489	R-PLACE1005066	9464
PLACE1005077	F-PLACE1005077	4490	R-PLACE1005077	9465
PLACE1005085	F-PLACE1005085	4491	R-PLACE1005085	9466
PLACE1005086	F-PLACE1005086	4492	R-PLACE1005086	9467
PLACE1005101	F-PLACE1005101	4493	R-PLACE1005101	9468
PLACE1005102	F-PLACE1005102	4494	R-PLACE1005102	9469
PLACE1005108	F-PLACE1005108	4495	R-PLACE1005108	9470
PLACE1005111	F-PLACE1005111	4496	R-PLACE1005111	9471
PLACE1005128	F-PLACE1005128	4497	R-PLACE1005128	9472
PLACE1005146	F-PLACE1005146	4498	R-PLACE1005146	9473
PLACE1005162	F-PLACE1005162	4499	R-PLACE1005162	9474
PLACE1005176	F-PLACE1005176	4500	R-nnnnnnnnnnnn	9475
PLACE1005181	F-PLACE1005181	4501	R-PLACE1005181	9476
PLACE1005187	F-PLACE1005187	4502	R-PLACE1005187	9477
PLACE1005206	F-PLACE1005206	4503	R-PLACE1005206	9478
PLACE1005232	F-PLACE1005232	4504	R-PLACE1005232	9479
PLACE1005243	F-PLACE1005243	4505	R-PLACE1005243	9480
PLACE1005261	F-PLACE1005261	4506	R-PLACE1005261	9481
PLACE1005266	F-PLACE1005266	4507	R-PLACE1005266	9482
PLACE1005277	F-PLACE1005277	4508	R-PLACE1005277	9483
PLACE1005287	F-PLACE1005287	4509	R-PLACE1005287	9484
PLACE1005305	F-PLACE1005305	4510	R-PLACE1005305	9485
PLACE1005308	F-PLACE1005308	4511	R-PLACE1005308	9486
PLACE1005313	F-PLACE1005313	4512	R-PLACE1005313	9487
PLACE1005327	F-PLACE1005327	4513	R-PLACE1005327	9488
PLACE1005331	F-PLACE1005331	4514	R-PLACE1005331	9489
PLACE1005335	F-PLACE1005335	4515	R-PLACE1005335	9490
PLACE1005373	F-PLACE1005373	4516	R-PLACE1005373	9491
PLACE1005374	F-PLACE1005374	4517	R-PLACE1005374	9492
PLACE1005409	F-PLACE1005409	4518	R-PLACE1005409	9493
PLACE1005453	F-PLACE1005453	4519	R-PLACE1005453	9494
PLACE1005467	F-PLACE1005467	4520	R-PLACE1005467	9495
PLACE1005471	F-PLACE1005471	4521	R-PLACE1005471	9496
PLACE1005477	F-PLACE1005477	4522	R-PLACE1005477	9497
PLACE1005480	F-PLACE1005480	4523	R-PLACE1005480	9498

NT2RP2001214	F-NT2RP2001214	16136	R-NT2RP2001214	16190
NT2RP2001460	F-NT2RP2001460	16137	R-NT2RP2001460	16191
NT2RP2001756	F-NT2RP2001756	16138	R-NT2RP2001756	16192
NT2RP2002056	F-NT2RP2002056	16139	R-NT2RP2002056	16193
NT2RP2002677	F-NT2RP2002677	16140	R-NT2RP2002677	16194
NT2RP2002755	F-NT2RP2002755	16141	R-NT2RP2002755	16195
NT2RP2002843	F-NT2RP2002843	16142	R-NT2RP2002843	16196
NT2RP2003101	F-NT2RP2003101	16143	R-NT2RP2003101	16197
NT2RP2003799	F-NT2RP2003799	16144	R-NT2RP2003799	16198
NT2RP2004095	F-NT2RP2004095	16145	R-NT2RP2004095	16199
NT2RP2004732	F-NT2RP2004732	16146	R-NT2RP2004732	16200
NT2RP2004920	F-NT2RP2004920	16147	R-NT2RP2004920	16201
NT2RP2005454	F-NT2RP2005454	16148	R-NT2RP2005454	16202
NT2RP2005776	F-NT2RP2005776	16149	R-NT2RP2005776	16203
NT2RP2005806	F-NT2RP2005806	16150	R-NT2RP2005806	16204
NT2RP2005882	F-NT2RP2005882	16151	R-NT2RP2005882	16205
NT2RP3001282	F-NT2RP3001282	16152	R-NT2RP3001282	16206
NT2RP3001723	F-NT2RP3001723	16153	R-NT2RP3001723	16207
NT2RP3002099	F-NT2RP3002099	16154	R-NT2RP3002099	16208
NT2RP3003155	F-NT2RP3003155	16155	R-NT2RP3003155	16209
NT2RP3004028	F-NT2RP3004028	16156	R-NT2RP3004028	16210
OVARC1000008	F-OVARC1000008	16157	R-OVARC1000008	16211
OVARC1000724	F-OVARC1000724	16158	R-OVARC1000724	16212
OVARC1000751	F-OVARC1000751	16159	R-OVARC1000751	16213
OVARC1001029	F-OVARC1001029	16160	R-OVARC1001029	16214
PLACE1000814	F-PLACE1000814	16161	R-PLACE1000814	16215
PLACE1003030	F-PLACE1003030	16162	R-PLACE1003030	16216
PLACE1005549	F-PLACE1005549	16163	R-PLACE1005549	16217
PLACE1007218	F-PLACE1007218	16164	R-PLACE1007218	16218

[0019] Furthermore, the present invention relates to the use of the above primers, as described below.

(4) A polynucleotide which can be synthesized with the primer set of (2) or (3).
(5) A polynucleotide comprising a coding region in the polynucleotide of (4).
(6) A substantially pure protein encoded by polynucleotide of (4).
(7) A partial peptide of the protein of (6).

[0020] In addition, the present invention comprises a polynucleotide described below and a protein encoded by the polynucleotide.

(8) An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351;
(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence

selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351, and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351;

(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);

(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351.

(9). A substantially pure protein encoded by the polynucleotide of (8).

(10) An antibody against the protein or peptide of any one of (6), (7), and (9).

(11) A vector comprising the polynucleotide of (5) or (8).

(12) A transformant carrying the polynucleotide of (5) or (8), or the vector of (11).

(13) A transformant expressively carrying the polynucleotide of (5) or (8), or the vector of (11).

(14) A method for producing the protein or peptide of any one of (6), (7), and (9), comprising culturing the transformant of (13) and recovering the expression product.

(15) An oligonucleotide comprising the nucleotide sequence set forth in any one of the SEQ ID NOs in Tables 350 and 351 or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

(16) Use of the oligonucleotide of (15) as a primer for synthesizing a polynucleotide.

(17) Use of the oligonucleotide of (15) as a probe for detecting a gene.

(18) An antisense polynucleotide against the polynucleotide of (8), or the portion thereof.

(19) A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of (2) or (3), or the primer of (16); and

b) recovering the synthesized product.

(20) The method of (19), wherein the cDNA library is obtainable by oligo-capping method.

(21) The method of (19), wherein the complementary strand is obtainable by PCR.

(22) A method for detecting the polynucleotide of (8), the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of (15) under the conditions where hybridization occurs, and

b) detecting the hybridization of the target polynucleotide with the oligonucleotide of (15).

(23) A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences set forth in the SEQ ID NOs in Tables 350 and 351 and/or the amino acid sequences set forth in the SEQ ID NOs in Tables 350 and 351, or a medium on which the database is stored.

[0021] Any patents, patent applications, and publications cited herein are incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] Figure 1 shows the restriction maps of vectors pME18SFL3 and pUC19FL3.

[0023] Figure 2 shows the reproducibility of gene expression analysis. The respective intensities of gene expression observed in independent set of experiments are plotted in the vertical axis as well as in the horizontal axis.

[0024] Figure 3 shows the detection limit in gene expression analysis. The intensity of expression is shown in the vertical axis and the concentration (μg/ml) of probe used is shown in the horizontal axis.

DETAILED DESCRIPTION OF THE INVENTION

[0025] Herein, "polynucleotide" is defined as a molecule in which multiple nucleotides are polymerized. There are no limitations in the number of the polymerized nucleotides. In case that the polymer contains relatively low number

of nucleotides, it is also described as an "oligonucleotide". The polynucleotide or the oligonucleotide of the present invention can be a natural or chemically synthesized product. Alternatively, it can be synthesized using a template DNA by an enzymatic reaction such as PCR.

[0026] All the cDNA provided by the invention are full-length cDNA. Herein, a "full-length cDNA" is defined as a cDNA which contains both ATG codon (the translation start site) and the stop codon. Accordingly, the untranslated regions, which are originally found in the upstream or downstream of the protein coding region in natural mRNA, may or may not be contained.

[0027] An "isolated polynucleotide" is a polynucleotide the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example,

(a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs;

(b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA;

(c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and

(d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein. Specifically excluded from this definition are nucleic acids present in mixtures of different (i) DNA molecules, (ii) transfected cells, or (iii) cell clones: e.g., as these occur in a DNA library such as a cDNA or genomic DNA library.

[0028] The term "substantially pure" as used herein in reference to a given polypeptide means that the protein or polypeptide is substantially free from other biological macromolecules. The substantially pure protein or polypeptide is at least 75% (e.g., at least 80, 85, 95, or 99%) pure by dry weight. Purity can be measured by any appropriate standard method, for example, by column chromatography, polyacrylamide gel electrophoresis, or HPLC analysis.

[0029] All the clones (5602 clones) of the present invention are novel and encode the full-length proteins. All the clones were prepared by oligo capping method, which can achieve cDNA cloning with high fullness ratio. The cDNA clones were selected by using ATGprl score as an index of the fullness ratio at the 5'-end, based on the sequence features of the 5'-end sequences. Selection was further carried out by searching GenBank database for EST sequences homologous to 5'-end sequence of each clone by BLAST [S.F. Altschul, W. Gish, W. Miller, E.W. Myers & D.L. Lipman J. Mol. Biol., 215:403-410 (1990); W. Gish, & D.J. States, Nature Genet., 3:266-272 (1993)] and by considering the number of matching (identical) EST sequences or the number of continuous amino acids in the 5'-end sequence initiated from the initiation codon.

[0030] Moreover, the clones were turn out to be not identical to any of the known human mRNA (namely novel) by homology search using the 5'-end sequence.

[0031] The primers of the present invention, which are used for synthesizing full-length cDNA, are selected from the group comprising SEQ ID NO: 1-5547 (5'-primer), or SEQ ID NO: 5548-10463 (3'-primer). Further, the primers of the present invention, which are used for synthesizing full-length cDNA, are selected from SEQ ID NO: 16111-16164 (5'-primer), or SEQ ID NO: 16165-16218 (3'-primer). Some of the nucleotides include a known EST as its part. However, the primers of the present invention are novel in terms that the primers enable to synthesize full-length cDNA. Because the known ESTs lack important information on what part of cDNA the ESTs correspond to, it is impossible to design primers on the basis of the ESTs.

[0032] All the full-length cDNA of the present invention can be synthesized using a primer set comprising the nucleotide sequences selected from both the 5'-and 3'-end sequences, or a set comprising a primer based on the 5'-end sequence and an oligo-dT primer, by a method such as PCR (Current protocols in Molecular Biology (1987) Ausubel et al. edit, John Wiley & Sons, Section 6.1-6.4).

[0033] Specifically, PCR can be performed using an oligonucleotide that has 15 nucleotides longer, and specifically hybridizes with the complementary strand of the polynucleotide that contains the nucleotide sequence selected from the 5'-end sequences shown in Table 1 and 2 (SEQ ID NO: 1-5547, or SEQ ID NO: 16111-16164), and an oligo-dT primer as a 5'-, and 3'-primer, respectively. The length of the primers is usually 15-100 bp, and favorably between 15-35 bp. In case of LA PCR, which is described below, the primer length of 25-35 bp may provide a good result.

[0034] A method to design a primer that enables a specific amplification based on the given nucleotide sequence is known to those skilled in the art (Current Protocols in Molecular Biology, Ausubel et al. edit, (1987) John Wiley & Sons, Section 6.1-6.4). In designing a primer based on the 5'-end sequence, the primer is designed so as that, in principle, the amplification products will include the translation start site. Accordingly, in case that a given 5'-end nucleotide sequence is the 5'- untranslated region (5'UTR), any part of the sequence can be used as a 5'-primer as far as the specificity toward the target cDNA is insured. The translation start site can be predicted using a known method such

as the ATGpr as described below.

[0035] When synthesizing a polynucleotide, the target nucleotide sequence to be amplified can extend to several thousand bp in some cDNA. However, it is possible to amplify such a long nucleotides by using such as LA PCR (Long and Accurate PCR). It is advantageous to use LA PCR when synthesizing long DNA. In LA PCR, in which a special DNA polymerase having 3'→5' exonuclease activity is used, misincorporated nucleotides can be removed. Accordingly, accurate synthesis of the complementary strand can be achieved even with a long nucleotide sequence. By using LA PCR, it is reported that amplification of a nucleotide with 20 kb longer can be achieved under desirable condition (Takeshi Hayashi (1996) Jikken-Igaku Bessatsu, "Advanced Technologies in PCR" Youdo-sha).

[0036] A template DNA for synthesizing the cDNA of the present invention can be obtained by using cDNA libraries that are prepared by various methods. The full-length cDNA clones obtained here are those with high fullness ratio, which were obtained using a combination of (1) a method to prepare a full-length-enriched cDNA library using the oligo-capping method, and (2) an estimation system for fullness using the 5'-end sequence (selection based on the estimation by the ATGpr after removing clones that are not-full-length compared to the ESTs). However, it is possible to easily obtain a full-length cDNA by using the primers that are provided by the present invention, not by the above described specialized method.

The problem with the cDNA libraries prepared by the known methods or commercially available is that mRNA contained in the libraries has very low fullness ratio. Thus, it is difficult to screen full-length cDNA clone directly from the library using ordinary cloning methods. The present invention has revealed a primer that is capable of synthesizing a full-length cDNA. If provided with primers, it is possible to synthesize a target full-length cDNA by using enzymatic reactions such as PCR. In particular, a full-length-enriched cDNA library, synthesized by methods such as oligo-capping, is desirable to synthesize a full-length cDNA with more reliability.

[0037] The 5'-end sequence of the full-length cDNA clones of the invention can be used to isolate the regulatory element of transcription including the promoter on the genome. By the spring of the year 2000, a rough draft of the human genome (analysis of human genomic sequence with lower accuracy), which covers 90% of the genome, is planned to be accomplished, and by the year 2003, analysis of the entire human genomic sequence is going to be finished. However, it is hard to analyze with software the transcription start sites on the human genome, in which long introns exist. By contrast, it is easy to specify the transcription start site on the genomic sequence using the 5'-end sequence of the full-length cDNA clone, thus it is easy to obtain the genomic region involved in transcription regulation, which includes the promoter that is contained in the upstream of the transcription start site.

[0038] The full-length cDNAs cloned in the present invention are classified into 13 groups, based on the data such as ATGpr1 score, by which the fullness ratio can be evaluated. Specifically, the 13 groups consist of; the below-mentioned groups (1)-(3), containing 3690 clones (Table 9), and the group (12), containing 3 clones, wherein ATGpr1 (score defined in the ATGpr program) is higher than 0.3; and the below-mentioned groups (4)-(11), containing 1857 clones (Table 10), and the group (13), containing 52 clones, wherein, although ATGpr1 is 0.3 or less, the clones are judged to be full-length from various viewpoints. Names of the clones belonging to the groups (1)-(13) are as indicated in Examples or below.

(1) 1516 clones

Among the 3690 clones that have the maximal ATGpr1 score higher than 0.3, 1516 clones are novel full-length clones, in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(2)377 clones

Among the 3690, 377 clones are novel full-length clones, in which the number of human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(3) 1797 clones

Among the 3690, 1797 clones are novel full-length clones, in which the number of human EST having identical sequence at the 5'-end is not more than 20 (except the clones described above).

(4) 453 clones

Among the 1857 clones in which the maximal ATGpr1 score is 0.3 or less, the following 453 clones are estimated to be novel full-length clones since the clones have the maximal score 0.3 or more in the ATGpr2, and at least either of the sequences of their 5'- and 3'-ends, or both are not identical to those of any human EST. The ATGpr2 score is determined by using the ATGpr program with neglecting the information of the frequency of the six nucleotides contained within the sequence between the ATG codon and the stop codon (the maximal length is 300 nucleotides from the ATG codon) (Salamo A.A., Nishikawa T., and Swindells M.B. (1998) Bioinformatics, 14: 384-390; http://www.hri.co.jp/atgpr/). The ATGpr program for calculating the ATGpr2 score is described as the

ATGpr2 program in the followings.

(5) 24 clones

Among the 1857 clones, 24 clones are estimated to be full-length since their maximal ATGpr2 scores are higher than 0.3, and also novel, though they have low scores in ATGpr1 program, in which the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(6) 65 clones

Among the 1857 clones, 65 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(7) 32 clones

Among the 1857 clones, 32 clones are estimated to be full-length since, though they have low scores in both programs, ATGpr1 and ATGpr2, the scores are the maximum in comparison to those of the other clones in the same cluster (at least two clones). The clones are also novel, if the number of the human EST having identical sequence at both 5'- and 3'-ends is 1 to 5.

(8) 36 clones

Among the 1857 clones, 36 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST.

(9) 81 clones

Among the 1857 clones, 81 clones are full-length, which were selected by assembling the sequences of the other clones or human EST, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if the number of the human EST having identical sequence at the 5'-end is not more than 20 (other than the clones in which at least either of the sequences of the 5'- and 3'-ends, or both are not identical to those of any human EST).

(10) 938 clones

Among the 1857 clones, 938 clones are estimated to be full-length according to the fullness ratio shown in Table 4, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 5'-end is not identical to those of any human EST.

(11) 228 clones

Among the 1857 clones, 228 clones are estimated to be full-length according to the fullness ratio shown in Table 7, although they have low scores in both programs, ATGpr1 and ATGpr2. The clones are also novel, if at least the sequence of the 3'-end is not identical to those of any human EST.

(12) 3 clones

Three clones, HEMBA1006812, HEMBB1001871, and NT2RP3001282, whose maximal ATGpr1 values are higher than 0.3, are full-length and novel clones whose 5'-end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 100 amino acids or more.

(13) 52 clones

The following 52 clones, which have maximal ATGpr1 values of 0.3 or less, are full-length with the fullness ratios shown in Table 4 although the fullness ratios are low:

HEMBA1000497, HEMBA1001750, HEMBA1003854, HEMBA1004193, HEMBA1004860, HEMBA1005572, HEMBA1006038, HEMBA1006092, HEMBA1006406, HEMBA1006650, HEMBB1000672, HEMBB1001197, MAMMA1001252, MAMMA1002094, NT2RM4000634, NT2RM4000657, NT2RM4000783, NT2RM4000857, NT2RM4001178, NT2RM4002420, NT2RP2000198, NT2RP2000551, NT2RP2000660, NT2RP2001214, NT2RP2001460, NT2RP2001756, NT2RP2002056, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2003101, NT2RP2003799, NT2RP2004095, NT2RP2004732, NT2RP2004920, NT2RP2005454, NT2RP2005776, NT2RP2005806, NT2RP2005882, NT2RP3001723, NT2RP3002099, NT2RP3003155, NT2RP3004028, OVARC1000008, OVARC1000724, OVARC1000751, OVARC1001029, PLACE1000814,

PLACE1003030, PLACE1005549, PLACE1007218, NT2RP4002298.

Moreover, the clones are novel clones whose 5' -end sequences presumably contain a coding region which is initiated with ATG codon and which encodes 50 amino acids or more. Among them, the following 20 clones is predicted to contain a coding region with 100 amino acids or more and should encode proteins:

HEMBA1000497, HEMBA1003854, HEMBA1004193, NT2RM4000657, NT2RM4001178, NT2RP2001756, NT2RP2002677, NT2RP2002755, NT2RP2002843, NT2RP2004095, NT2RP2004920, NT2RP2005806, NT2RP3002099, NT2RP3003155, OVARC1000724, OVARC1001029, PLACE1000814, PLACE1003030, PLACE1005549, PLACE1007218.

[0039] The protein encoded by the polynucleotide of the invention can be prepared as a recombinant protein or as a natural protein. For example, the recombinant protein can be prepared by inserting the polynucleotide encoding the protein of the invention into a vector, introducing the vector into an appropriate host cell and purifying the protein expressed within the transformed host cell, as described below. In contrast, the natural protein can be prepared, for example, by utilizing an affinity column to which an antibody against the protein of the invention (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 16.1-16.19) is attached. The antibody used for affinity purification may be either a polyclonal antibody, or a monoclonal antibody. Alternatively, in vitro translation (See, for example, "On the fidelity of mRNA translation in the nuclease-treated rabbit reticulocyte lysate system." Dasso M.C., and Jackson R.J. (1989) Nucleic Acids Res. 17: 3129-3144) may be used for preparing the protein of the invention.

[0040] Proteins functionally equivalent to the proteins of the present invention can be prepared based on the activities, which were clarified in the above-mentioned manner, of the proteins of the present invention. Using the biological activity possessed by the protein of the invention as an index, it is possible to verify whether or not a particular protein is functionally equivalent to the protein of the invention by examining whether or not the protein has said activity.

[0041] Proteins functionally equivalent to the proteins of the present invention can be prepared by those skilled in the art, for example, by using a method for introducing mutations into an amino acid sequence of a protein (for example, site-directed mutagenesis (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 8.1-8.5). Besides, such proteins can be generated by spontaneous mutations. The present invention comprises the proteins having one or more amino acids substitutions, deletions, insertions and/or additions in the amino acid sequences of the proteins of the present invention (Tables 350 and 351), as far as the proteins have the equivalent functions to those of the proteins identified in the present Examples described later.

[0042] There are no limitations in the number and sites of amino acid mutations, as far as the proteins maintain the functions thereof. The number of mutations is typically 30% or less, or 20% or less, or 10% or less, preferably within 5% or less, or 3% or less of the total amino acids, more preferably within 2% or less or 1 % or less of the total amino acids. From the viewpoint of maintaining the protein function, it is preferable that a substituted amino has a similar property to that of the original amino acid. For example, Ala, Val, Leu, Ile, Pro, Met, Phe and Trp are assumed to have similar properties to one another because they are all classified into a group of non-polar amino acids. Similarly, substitution can be performed among non-charged amino acid such as Gly, Ser, Thr, Cys, Tyr, Asn, and Gln, acidic amino acids such as Asp and Glu, and basic amino acids such as Lys, Arg, and His.

[0043] In addition, proteins functionally equivalent to the proteins of the present invention can be isolated by using techniques of hybridization or gene amplification known to those skilled in the art. Specifically, using the hybridization technique (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)), those skilled in the art can usually isolate a DNA highly homologous to the DNA encoding the protein identified in the present Example based on the identified nucleotide sequence (Tables 350 and 351) or a portion thereof and obtain the functionally equivalent protein from the isolated DNA. The present invention include proteins encoded by the DNAs hybridizing with the DNAs encoding the proteins identified in the present Example, as far as the proteins are functionally equivalent to the proteins identified in the present Example. Organisms from which the functionally equivalent proteins are isolated are illustrated by vertebrates such as human, mouse, rat, rabbit, pig and bovine, but are not limited to these animals.

[0044] Washing conditions of hybridization for the isolation of DNAs encoding the functionally equivalent proteins are usually "1 × SSC, 0.1% SDS, 37°C"; more stringent conditions are "0.5 × SSC, 0.1% SDS, 42°C"; and still more stringent conditions are "0.1 × SSC, 0.1% SDS, 65°C". Alternatively, the following conditions can be given as hybridization conditions of the present invention. Namely, conditions in which the hybridization is done at "6 × SSC, 40% Formamide, 25°C", and the washing at "1 × SSC, 55°C" can be given. More preferable conditions are those in which the hybridization is done at "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". Even more preferable are those in which the hybridization is done at "6 × SSC, 50% Formamide, 37°C", and the washing at "0.1 × SSC, 62°C". The more stringent the conditions of hybridization are, the more frequently the DNAs highly homologous to the probe sequence are isolated. Therefore, it is preferable to conduct hybridization under stringent conditions. Examples of stringent conditions in the present invention are, washing conditions of "0.5 × SSC, 0.1% SDS, 42°C", or alternatively, hybridization conditions of "6 × SSC, 40% Formamide, 37°C", and the washing at "0.2 × SSC, 55°C". However, the above-mentioned combinations of SSC, SDS and temperature conditions are indicated just as examples.

Those skilled in the art can select the hybridization conditions with similar stringency to those mentioned above by properly combining the above-mentioned or other factors (for example, probe concentration, probe length and duration of hybridization reaction) that determines the stringency of hybridization.

[0045] The amino acid sequences of proteins isolated by using the hybridization techniques usually exhibit high homology to those of the proteins of the present invention, which are shown in Tables 350 and 351. The present invention encompasses a polynucleotide comprising a nucleotide sequence that has a high identity to the nucleotide sequence of claim 8 (a).

Furthermore, the present invention encompasses a peptide, or protein comprising an amino acid sequence that has a high identity to the amino acid sequence encoded by the polynucleotide of claim 8 (b). The term "high identity" indicates sequence identity of at least 40% or more;

preferably 60% or more; and more preferably 70% or more. Alternatively, more preferable is identity of 90% or more, or 93% or more, or 95% or more, furthermore, 97% or more, or 99% or more. The identity can be determined by using the BLAST search algorithm.

[0046] With the gene amplification technique (PCR) (Current Protocols in Molecular Biology, edit, Ausubel et al., (1987) John Wiley & Sons, Section 6.3-6.4)) using primers designed based on the nucleotide sequence (Tables 350 and 351) or a portion thereof identified in the present Example, it is possible to isolate a DNA fragment highly homologous to the polynucleotide sequence or a portion thereof and to obtain functionally equivalent protein to a particular protein identified in the present Example based on the isolated DNA fragment.

[0047] The "percent identity" of two amino acid sequences or of two nucleic acids is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sei. USA 87:2264-2268, 1990), modified as in Karlin and Altschul (Proc. Natl. Acad. Sei. USA 90:5873-5877, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol.215:403-410, 1990). BLAST nucleotide searches are performed with the BLASTN program, score = 100, wordlength = 12. BLAST protein searches are performed with the BLASTX program, score = 50, wordlength = 3. When gaps exist between two sequences, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res.25:3389-3402,1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are used. See http://www.ncbi.nlm.nih.gov.

[0048] The present invention also includes a partial peptide of the proteins of the invention. The partial peptide comprises a protein generated as a result that a signal peptide has been removed from a secretory protein. If the protein of the present invention has an activity as a receptor or a ligand, the partial peptide may function as a competitive inhibitor of the protein and may bind to the receptor (or ligand). In addition, the present invention comprises an antigen peptide for raising antibodies. For the peptides to be specific for the protein of the invention, the peptides comprise at least 7 amino acids, preferably 8 amino acids or more, more preferably 9 amino acids or more, and even more preferably 10 amino acids or more. The peptide can be used for preparing antibodies against the protein of the invention, or competitive inhibitors of them, and also screening for a receptor that binds to the protein of the invention. The partial peptides of the invention can be produced, for example, by genetic engineering methods, known methods for synthesizing peptides, or digesting the protein of the invention with an appropriate peptidase.

[0049] The present invention also relates to a vector into which the DNA of the invention is inserted. The vector of the invention is not limited as long as it contains the inserted DNA stably. For example, if *E. coli* is used as a host, vectors such as pBluescript vector (Stratagene) are preferable as a cloning vector. To produce the protein of the invention, expression vectors are especially useful. Any expression vector can be used as far as it is capable of expressing the protein *in vitro,* in *E. coli,* in cultured cells, or *in vivo.* For example, pBEST vector (Promega) is preferable for *in vitro* expression, pET vector (Invitrogen) for *E. coli,* pME18S-FL3 vector (GenBank Accession No. AB009864) for cultured cells, and pME18S vector (Mol. Cell. Biol. (1988) 8: 466-472) for *in vivo* expression. To insert the DNA of the invention, ligation utilizing restriction sites can be performed according to the standard method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0050] The present invention also relates to a transformant carrying the vector of the invention. Any cell can be used as a host into which the vector of the invention is inserted, and various kinds of host cells can be used depending on the purposes. For strong expression of the protein in eukaryotic cells, COS cells or CHO cells can be used, for example.

[0051] Introduction of the vector into host cells can be performed, for example, by calcium phosphate precipitation method, electroporation method (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 9.1-9.9), lipofectamine method (GIBCO-BRL), or microinjection method, etc.

[0052] The primer of the present invention can be used for synthesizing full-length cDNA, and also for the detection and/or diagnosis of the abnormality of the protein of the invention encoded by the full-length cDNA. For example, by utilizing polymerase chain reaction (genomic DNA-PCR, or RT-PCR) using the primer of the invention, DNA encoding the protein of the invention can be amplified. It is also possible to obtain the regulatory region of expression in the 5'-upstream by using PCR or hybridization since the transcription start site within the genomic sequence can be easily specified based on the 5'-end sequence of the full-length cDNA. The obtained genomic region can be used for detection and/or diagnosis of the abnormality of the sequence by RFLP analysis, SSCP, or direct sequencing.

[0053] Furthermore, the "polynucleotide having a length of at least 15 nucleotides, comprising a nucleotide sequence that is complementary to a polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs in Tables 350 and 351, or its complementary strand" includes an antisense polynucleotide for suppressing the expression of the protein of the invention. To exert the antisense effect, the antisense polynucleotide has a length of at least 15 bp or more, for example, 50 bp or more, preferably 100 bp or more, and more preferably 500 bp or more, and has a length of usually 3000 bp or less and preferably 2000 bp or less. The antisense DNA can be used in the gene therapy of the diseases that are caused by the abnormality of the protein of the invention (abnormal function or abnormal expression). Said antisense DNA can be prepared, for example, by the phosphorothioate method ("Physicochemical properties of phosphorothioate oligodeoxynucleotides." Stein (1988) Nucleic Acids Res. 16: 3209-3221) based on the nucleotide sequence of the DNA encoding the protein (for example, the DNA set forth in any one of SEQ ID NOs in Tables 350 and 351).

[0054] The polynucleotide or antisense DNA of the present invention can be used in gene therapy, for example, by administrating it into a patient by the in vivo or ex vivo method with virus vectors such as retrovirus vectors, adenovirus vectors, and adeno-associated virus vectors, or non-virus vectors such as liposome.

[0055] The present invention also relates to antibodies that bind to the protein of the invention.
There are no limitations in the form of the antibodies of the invention. They include polyclonal antibodies, monoclonal antibodies, or their portions that can bind to the protein of the invention. They also include antibodies of all classes. Furthermore, special antibodies such as humanized antibodies are also included.

[0056] The polyclonal antibody of the invention can be obtained according to the standard method by synthesizing an oligopeptide corresponding to the amino acid sequence and immunizing rabbits with the peptides (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.12-11.13). The monoclonal antibody of the invention can be obtained according to the standard method by purifying the protein expressed in *E. coli,* immunizing mice with the protein, and producing a hybridoma cell by fusing the spleen cells and myeloma cells (Current Protocols in Molecular Biology (1987) Ausubel et al. edit, John Wily & Sons, Section 11.4-11.11).

[0057] The antibody binding to the protein of the present invention can be used for purification of the protein of the invention, and also for detection and/or diagnosis of the abnormalities of the expression and structure of the protein. Specifically, proteins can be extracted, for example, from tissues, blood, or cells, and the protein of the invention is detected by Western blotting, immunoprecipitation, or ELISA, etc. for the above purpose.

[0058] Furthermore, the antibody binding to the protein of the present invention can be utilized for treating the diseases that associates with the protein of the invention. If the antibodies are used for treating patients, human antibodies or humanized antibodies are preferable in terms of their low antigenicity. The human antibodies can be prepared by immunizing a mouse whose immune system is replaced with that of human ("Functional transplant of megabase human immunoglobulin loci recapitulates human antibody response in mice" Mendez M.J. et al. (1997) Nat. Genet. 15: 146-156). The humanized antibodies can be prepared by recombination of the hypervariable region of a monoclonal antibody (Methods in Enzymology (1991) 203: 99-121).

[0059] The cDNA of the present invention encodes the amino acid sequence of a protein which is predicted to have the function(s) described below based on the homology search of the GenBank and SwissProt. Specifically, for instance, as shown in EXAMPLES, searching a known gene or protein that is homologous to the partial sequence of the full-length cDNA of the invention (5602 clone) and referring the function of the gene and of the protein encoded by the gene make it possible to predict the function of the protein encoded by the cDNA of the invention. In this way, each of 1437 clones out of the 5602 full-length cDNA clones of the invention was predicted to encode a protein that was classified into one or more of the following categories.

Secretory or membrane protein (261 clones)
Glycoprotein-associated protein (113 clones)
Signal transduction-associated protein (148 clones)
Transcription-associated protein (233 clones)
Disease-associated protein (437 clones)
Enzyme or metabolism-associated protein (301 clones)
Cell division- or cell proliferation-associated protein (74 clones)
Cytoskeleton-associated protein (92 clones)
RNA synthesis-associated protein (280 clones)
Nuclear protein (352 clones)
Protein synthesis- or transport-associated protein (112 clones)
Cellular defense-associated protein (23 clones)
Development- or growth-associated protein (23 clones)

[0060] It is also possible to predict the protein function by looking into the amino acid sequence for the motifs such

as the signal sequence, transmembrane region, nuclear translocation signal, glycosylation signal, phosphorylation site, Zinc finger motif, and SH3 domain. The programs, PSORT (Nakai K., and Kanehisa M. (1992) Genomics 14: 897-911), SOSUI (Hirokawa T. et al. (1998) Bioinformatics 14: 378-379) (Mitsui Information Developing Inc.), and MEMSAT (Jones D.T., Taylor W.R., and Thornton J.M. (1994) Biochemistry 33: 3038-3049) can be used to predict the existence of the signal sequence or transmembrane region. Alternatively, a partial amino acid sequence of the protein is fused with another protein such as GFP, the fusion protein is transfected into cultured cells, and the localization is analyzed to predict the function of the original protein.

[0061] Based on the determined nucleotide sequences of the full-length cDNAs obtained in the present invention, it is possible to predict more detailed functions of the proteins encoded by the cDNA clones, for example, by searching the databases such as GenBank, Swiss-Prot and UniGene for homologies of the cDNAs; or by searching the amino acid sequences deduced from the full-length cDNAs for signal sequences by using software programs such as PSORT, for transmembrane regions by using software programs such as SOSUI or for motifs by using software programs such as Pfam (http://www.sanger.ac.uk/Software/Pfam/index.shtm1) and PROSITE (http://www.expasy.ch/prosite/). As a matter of course, the functions are often predictable by using partial sequence information (preferably 300 nucleotides or more) instead of the full-length nucleotide sequences. However, the result of the prediction by using partial nucleotide sequence does not always agree with the result obtained by using full-length nucleotide sequence, and thus, it is needless to say that the prediction of function is preferably performed based on the full-length nucleotide sequences. GenBank, Swiss-Prot and UniGene databases were searched for homologies of the full-length nucleotide sequences of the 4997 clones (see Example 18). The amino acid sequences deduced from the full-length nucleotide sequences were searched for functional domains by PSORT, SOSUI and Pfam. Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on these results obtained.

The following 798 clones were categorized into secretory and/or membrane proteins.

HEMBA1000356, HEMBA1000518, HEMBA1000531, HEMBA1000637, HEMBA1000719, HEMBA1000817,
HEMBA1000822, HEMBA1000852, HEMBA1000870, HEMBA1000991, HEMBA1001052, HEMBA1001071,
HEMBA1001085, HEMBA1001286, HEMBA1001351, HEMBA1001407, HEMBA1001446, HEMBA1001515,
HEMBA1001557, HEMBA1001569, HEMBA1001661, HEMBA1001734, HEMBA1001746, HEMBA1001866,
HEMBA1002125, HEMBA1002150, HEMBA1002166, HEMBA1002417, HEMBA1002462, HEMBA1002475,
HEMBA1002477, HEMBA1002486, HEMBA1002609, HEMBA1002659, HEMBA1002661, HEMBA1002780,
HEMBA1002818, HEMBA1002876, HEMBA1002921, HEMBA1003071, HEMBA1003077, HEMBA1003079,
HEMBA1003086, HEMBA1003096, HEMBA1003281, HEMBA1003286, HEMBA1003538, HEMBA1003711,
HEMBA1003742, HEMBA1003803, HEMBA1004055, HEMBA1004143, HEMBA1004146, HEMBA1004207,
HEMBA1004341, HEMBA1004461, HEMBA1004577, HEMBA1004637, HEMBA1004752, HEMBA1004756,
HEMBA1004850, HEMBA1004889, HEMBA1004923, HEMBA1004930, HEMBA1005029, HEMBA1005035,
HEMBA1005050, HEMBA1005552, HEMBA1005576, HEMBA1005581, HEMBA1005588, HEMBA1005616,
HEMBA1005699, HEMBA1005991, HEMBA1006036, HEMBA1006038, HEMBA1006067, HEMBA1006173,
HEMBA1006198, HEMBA1006293, HEMBA1006310, HEMBA1006492, HEMBA1006502, HEMBA1006583,
HEMBA1006659, HEMBA1006758, HEMBA1006789, HEMBA1006921, HEMBA1006926, HEMBA1006976,
HEMBA1007203, HEMBA1007301, HEMBB1000037, HEMBB1000050, HEMBB1000054, HEMBB1000175,
HEMBB1000317, HEMBB1000556, HEMBB1000593, HEMBB1000631, HEMBB1000763, HEMBB1000827,
HEMBB1000915, HEMBB1000975, HEMBB1001112, HEMBB1001151, HEMBB1001177, HEMBB1001302,
HEMBB1001348, HEMBB1001564, HEMBB1001630, HEMBB1001871, HEMBB1001872, HEMBB1001925,
HEMBB1001962, HEMBB1002042, HEMBB1002044, HEMBB1002142, HEMBB1002190, HEMBB1002193,
HEMBB1002247, HEMBB1002383, HEMBB1002387, HEMBB1002550, HEMBB1002600, HEMBB1002692,
MAMMA1000045, MAMMA1000129, MAMMA1000133, MAMMA1000277, MAMMA1000278, MAMMA1000410,
MAMMA1000416, MAMMA1000472, MAMMA1000672, MAMMA1000684, MAMMA1000714, MAMMA1000734,
MAMMA1000778, MAMMA1000798, MAMMA1000842, MAMMA1000859, MAMMA1000897, MAMMA1000956,
MAMMA1001008, MAMMA1001030, MAMMA1001041, MAMMA1001073, MAMMA1001080, MAMMA1001139,
MAMMA1001154, MAMMA1001322, MAMMA1001388, MAMMA1001411, MAMMA1001487, MAMMA1001751,
MAMMA1001754, MAMMA1001771, MAMMA1002009, MAMMA1002427, MAMMA1002428, MAMMA1002461,
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[0062] The following 142 clones were categorized into glycoprotein-associated proteins.

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[0063] The following 140 clones were categorized into signal transduction-associated proteins.

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[0064] The following 321 clones were categorized into transcription -associated proteins.

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HEMBB1002342, HEMBB1002607, MAMMA1000183, MAMMA1000388, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001627, MAMMA1001633, MAMMA1001743, MAMMA1001820, MAMMA1001837, MAMMA1002617, MAMMA1002650, MAMMA1002937, NT2RM1000055, NT2RM1000086, NT2RM1000746, NT2RM1000885, NT2RM1000894, NT2RM1001092, NT2RM2000013, NT2RM2000452, NT2RM2000735, NT2RM2000740, NT2RM2001035, NT2RM2001105, NT2RM2001575, NT2RM2001670, NT2RM2001716,

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[0065] The following 392 clones were categorized into disease-associated proteins.

HEMBA1000020, HEMBA1000216, HEMBA1000304, HEMBA1000561, HEMBA1000569, HEMBA1000910, HEMBA1001043, HEMBA1001059, HEMBA1001071, HEMBA1001088, HEMBA1001569, HEMBA1001661, HEMBA1001672, HEMBA1001819, HEMBA1001921, HEMBA1002267, HEMBA1002419, HEMBA1002469, HEMBA1002547, HEMBA1002555, HEMBA1002810, HEMBA1002939, HEMBA1002997, HEMBA1003148, HEMBA1003369, HEMBA1003417, HEMBA1003418, HEMBA1003433, HEMBA1003538, HEMBA1003555, HEMBA1003568, HEMBA1003569, HEMBA1003581, HEMBA1004168, HEMBA1004202, HEMBA1004248, HEMBA1004275, HEMBA1004321, HEMBA1004353, HEMBA1004356, HEMBA1004479, HEMBA1004509, HEMBA1004669, HEMBA1005009, HEMBA1005338, HEMBA1005367, HEMBA1005423, HEMBA1005528, HEMBA1005581, HEMBA1005621, HEMBA1005699, HEMBA1006507, HEMBA1006650, HEMBA1006652, HEMBA1006737, HEMBA1006807, HEMBA1006877, HEMBA1007121, HEMBA1007243, HEMBB1000119, HEMBB1000693, HEMBB1000927, HEMBB1000985, HEMBB1001068, HEMBB1001282, HEMBB1001339, HEMBB1001482, HEMBB1001564, HEMBB1001802, HEMBB1001905, HEMBB1001908, HEMBB1002217, HEMBB1002477, MAMMA1000388, MAMMA1000731, MAMMA1001305, MAMMA1001633, MAMMA1001868, MAMMA1002170, MAMMA1002198, MAMMA1002268, MAMMA1002485, MAMMA1002530, MAMMA1002858, MAMMA1002869, MAMMA1002881, MAMMA1003047, MAMMA1003146, MAMMA1003166, NT2RM1000001, NT2RM1000153, NT2RM1000252, NT2RM1000555, NT2RM1000770, NT2RM1000826, NT2RM1000850, NT2RM1001003, NT2RM1001092, NT2RM1001102, NT2RM2000191, NT2RM2000363, NT2RM2000594, NT2RM2000624, NT2RM2000714, NT2RM2000821, NT2RM2001035, NT2RM2001575, NT2RM2001652, NT2RM2001664, NT2RM2001668, NT2RM2001698, NT2RM2001803, NT2RM2001839, NT2RM4000155, NT2RM4000471, NT2RM4000486, NT2RM4000657, NT2RM4000751, NT2RM4000996, NT2RM4001629, NT2RM4001810, NT2RM4001819, NT2RM4001865, NT2RM4001876, NT2RM4001940, NT2RM4002066, NT2RM4002093, NT2RM4002146, NT2RM4002161, NT2RM4002323, NT2RM4002558, NT2RM4002571, NT2RP1000086, NT2RP1000574, NT2RP1000738, NT2RP1000825, NT2RP1000833, NT2RP1000959, NT2RP1000966, NT2RP1001013, NT2RP1001185, NT2RP1001482, NT2RP1001665, NT2RP2000070, NT2RP2000147, NT2RP2000224, NT2RP2000248, NT2RP2000297, NT2RP2000310, NT2RP2000414, NT2RP2000420, NT2RP2000523, NT2RP2000809, NT2RP2000812, NT2RP2001233, NT2RP2001327, NT2RP2001378, NT2RP2001394, NT2RP2001397, NT2RP2001460,

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[0066] The following 427 clones presumably belong to enzymes and/or metabolism-associated proteins. HEMBA1000012, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000542, HEMBA1000852, HEMBA1001019, HEMBA1001257, HEMBA1001526, HEMBA1001620, HEMBA1001866, HEMBA1001896, HEMBA1002212, HEMBA1002513, HEMBA1002746, HEMBA1002973, HEMBA1003046, HEMBA1003136, HEMBA1003179, HEMBA1003250, HEMBA1003291, HEMBA1003408, HEMBA1003538, HEMBA1003679, HEMBA1003680, HEMBA1004199, HEMBA1004227, HEMBA1004408, HEMBA1004509, HEMBA1004734, HEMBA1004768, HEMBA1005394, HEMBA1005513, HEMBA1005737, HEMBA1005815, HEMBA1006031, HEMBA1006272, HEMBA1006278, HEMBA1006291, HEMBA1006309, HEMBA1006347, HEMBA1006485, HEMBA1006521, HEMBA1006624, HEMBA1006885, HEMBA1006976, HEMBA1007121, HEMBA1007224, HEMBA1007243, HEMBA1007300, HEMBB1000083, HEMBB1000217, HEMBB1000915, HEMBB1000947, HEMBB1001137, HEMBB1001346, HEMBB1001429, HEMBB1001443, HEMBB1001915, HEMBB1001950, HEMBB1002042, MAMMA1000020, MAMMA1000085, MAMMA1000672, MAMMA1000713, MAMMA1000841, MAMMA1000897, MAMMA1001008, MAMMA1001038, MAMMA1001059, MAMMA1001476, MAMMA1001501, MAMMA1002268, MAMMA1002470, MAMMA1002530, MAMMA1002573, MAMMA1002619, MAMMA1002655, MAMMA1002671, MAMMA1003013, MAMMA1003035, NT2RM1000039, NT2RM1000132, NT2RM1000153, NT2RM1000256, NT2RM1000280, NT2RM1000377, NT2RM1000553, NT2RM1000648, NT2RM1000702, NT2RM1000894, NT2RM1001072, NT2RM1001115, NT2RM2000013, NT2RM2000092, NT2RM2000322, NT2RM2000368, NT2RM2000371, NT2RM2000469, NT2RM2000504, NT2RM2000577, NT2RM2000594, NT2RM2000951, NT2RM2001238, NT2RM2001547, NT2RM2001632, NT2RM2001664, NT2RM2001698,

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[0067] The following 217 clones presumably belong to ATP- and/or GTP-binding proteins.

HEMBA1000012, HEMBA1000129, HEMBA1000185, HEMBA1000491, HEMBA1000531, HEMBA1001019, HEMBA1001174, HEMBA1001387, HEMBA1001595, HEMBA1001723, HEMBA1001913, HEMBA1002161, HEMBA1002212, HEMBA1002876, HEMBA1002997, HEMBA1003250, HEMBA1003291, HEMBA1003369,

HEMBA1003555, HEMBA1003560, HEMBA1004131, HEMBA1004199, HEMBA1004202, HEMBA1004354, HEMBA1004697, HEMBA1005047, HEMBA1005595, HEMBA1007018, HEMBA1007151, HEMBB1000083, HEMBB1000226, HEMBB1000264, HEMBB1000632, HEMBB1000725, HEMBB1001294, HEMBB1002193, MAMMA1000085, MAMMA1000612, MAMMA1000731, MAMMA1000738, MAMMA1001038, MAMMA1001735, MAMMA1001768, MAMMA1003127, NT2RM1000187, NT2RM1000388, NT2RM1000702, NT2RM1000772, NT2RM1000924, NT2RM2000469, NT2RM2000577, NT2RM2000740, NT2RM2001100, NT2RM2001201, NT2RM2001345, NT2RM2001823, NT2RM2002128, NT2RM4000155, NT2RM4000191, NT2RM4000356, NT2RM4000496, NT2RM4000611, NT2RM4000733, NT2RM4000820, NT2RM4001084, NT2RM4001178, NT2RM4001344, NT2RM4001444, NT2RM4001592, NT2RM4001714, NT2RM4001758, NT2RM4001880, NT2RM4002062, NT2RM4002174, NT2RM4002205, NT2RM4002527, NT2RM4002594, NT2RM4002623, NT2RP1000470, NT2RP1000478, NT2RP1000915, NT2RP1000958, NT2RP1001080, NT2RP1001410, NT2RP1001569, NT2RP2000126, NT2RP2000258, NT2RP2000329, NT2RP2000660, NT2RP2000668, NT2RP2000710, NT2RP2000812, NT2RP2000880, NT2RP2001245, NT2RP2001392, NT2RP2002606, NT2RP2003277, NT2RP2003912, NT2RP2004538, NT2RP2004568, NT2RP2004689, NT2RP2004768, NT2RP2004791, NT2RP2004920, NT2RP2005344, NT2RP2005393, NT2RP2005763, NT2RP2006534, NT2RP3000046, NT2RP3000252, NT2RP3000350, NT2RP3000359, NT2RP3000366, NT2RP3000397, NT2RP3000759, NT2RP3000845, NT2RP3000875, NT2RP3001150, NT2RP3001427, NT2RP3001453, NT2RP3001529, NT2RP3001730, NT2RP3001799, NT2RP3001857, NT2RP3001938, NT2RP3002007, NT2RP3002151, NT2RP3002330, NT2RP3002399, NT2RP3002671, NT2RP3003301, NT2RP3003353, NT2RP3003589, NT2RP3003809, NT2RP3003876, NT2RP3004189, NT2RP3004428, NT2RP3004578, NT2RP4000290, NT2RP4000481, NT2RP4000518, NT2RP4000781, NT2RP4000839, NT2RP4000929, NT2RP4001041, NT2RP4001079, NT2RP4001375, NT2RP4001414, NT2RP4001592, NT2RP4001634, NT2RP4001644, NT2RP4001656, NT2RP4001896, NT2RP4002047, NT2RP4002058, NT2RP4002408, NT2RP5003477, OVARC1000013, OVARC1000304, OVARC1000556, OVARC1000771, OVARC1000800, OVARC1001068, OVARC1002138, PLACE1000040, PLACE1000588, PLACE1001104, PLACE1001739, PLACE1002433, PLACE1002437, PLACE1002714, PLACE1003394, PLACE1003521, PLACE1003915, PLACE1004902, PLACE1005243, PLACE1005305, PLACE1005549, PLACE1005739, PLACE1005921, PLACE1006119, PLACE1006196, PLACE1006552, PLACE1006956, PLACE1007409, PLACE1007697, PLACE1007946, PLACE1008244, PLACE1009404, PLACE1009476, PLACE1009596, PLACE1009908, PLACE1010134, PLACE1010720, PLACE1010896, PLACE1011109, PLACE1011114, PLACE1011310, PLACE1011922, PLACE2000014, PLACE2000039, PLACE2000274, PLACE2000404, PLACE2000427, PLACE3000350, PLACE4000009, PLACE4000014, PLACE4000326, SKNMC1000013, THYRO1000072, THYRO1001458, Y79AA1000833, Y79AA1000962, Y79AA1001394, Y79AA1001875, Y79AA1001963, Y79AA1002209,

[0068] The following 320 clones presumably belong to nuclear proteins.

HEMBA1000005, HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001579, HEMBA1001809, HEMBA1001819, HEMBA1001824, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002241, HEMBA1002495, HEMBA1002569, HEMBA1002935, HEMBA1002951, HEMBA1002999, HEMBA1003408, HEMBA1003545, HEMBA1003662, HEMBA1003684, HEMBA1003690, HEMBA1003760, HEMBA1004203, HEMBA1004321, HEMBA1004353, HEMBA1004479, HEMBA1004973, HEMBA1005219, HEMBA1005359, HEMBA1005558, HEMBA1005931, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006485, HEMBA1007087, HEMBB1000226, HEMBB1000789, HEMBB1001011, HEMBB1001056, HEMBB1001242, HEMBB1001482, HEMBB1001915, HEMBB1002134, HEMBB1002217, MAMMA1000183, MAMMA1000731, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001633, MAMMA1001743, MAMMA1001837, MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000187, NT2RM1000666, NT2RM1000885, NT2RM1000894, NT2RM1001059, NT2RM1001092, NT2RM2000013, NT2RM2000588, NT2RM2000624, NT2RM2000735, NT2RM2000740, NT2RM2001105, NT2RM2001635, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001936, NT2RM2001989, NT2RM2002004, NT2RM2002088, NT2RM2002091, NT2RM4000024, NT2RM4000046, NT2RM4000104, NT2RM4000202, NT2RM4000215, NT2RM4000290, NT2RM4000531, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001200, NT2RM4001483, NT2RM4001566, NT2RM4001592, NT2RM4001597, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001979, NT2RP1000035, NT2RP1000111, NT2RP1000493, NT2RP1000574, NT2RP1000630, NT2RP1000902, NT2RP1000915, NT2RP1000958, NT2RP1000966, NT2RP1001013, NT2RP1001177, NT2RP2000008, NT2RP2000076, NT2RP2000126, NT2RP2000153, NT2RP2000161, NT2RP2000248, NT2RP2000258, NT2RP2000297, NT2RP2000420, NT2RP2000931, NT2RP2001233, NT2RP2001420, NT2RP2001756, NT2RP2001869, NT2RP2002079, NT2RP2002270, NT2RP2002503, NT2RP2002591, NT2RP2002880,

NT2RP2002939, NT2RP2002993, NT2RP2003137, NT2RP2003157, NT2RP2003277, NT2RP2003286, NT2RP2003308, NT2RP2003347, NT2RP2003714, NT2RP2003912, NT2RP2004013, NT2RP2004187, NT2RP2004689, NT2RP2004920, NT2RP2005393, NT2RP2005436, NT2RP2005496, NT2RP2005539, NT2RP2005701, NT2RP2005767, NT2RP2005776, NT2RP2005933, NT2RP2005942, NT2RP2006043, NT2RP2006436, NT2RP3000031, NT2RP3000050, NT2RP3000397, NT2RP3000512, NT2RP3000527, NT2RP3000590, NT2RP3000603, NT2RP3000632, NT2RP3000917, NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001253, NT2RP3001338, NT2RP3001384, NT2RP3001398, NT2RP3001427, NT2RP3001428, NT2RP3001472, NT2RP3001646, NT2RP3001671, NT2RP3001792, NT2RP3001855, NT2RP3002056, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003193, NT2RP3003212, NT2RP3003555, NT2RP3004016, NT2RP3004206, NT2RP3004424, NT2RP3004428, NT2RP3004566, NT2RP3004617, NT2RP4000078, NT2RP4000111, NT2RP4000210, NT2RP4000398, NT2RP4000481, NT2RP4000518, NT2RP4000997, NT2RP4001148, NT2RP4001206, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001638, NT2RP4001696, NT2RP4001753, NT2RP4001938, NT2RP4002058, NT2RP4002078, NT2RP4002081, NT2RP4002791, OVARC1000006, OVARC1000087, OVARC1000091, OVARC1000241, OVARC1000326, OVARC1000556, OVARC1000846, OVARC1001038, OVARC1001180, OVARC1001232, OVARC1001271, OVARC1001306, OVARC1001436, OVARC1002112, PLACE1000133, PLACE1000184, PLACE1000406, PLACE1000583, PLACE1000596, PLACE1000979, PLACE1001118, PLACE1001383, PLACE1001632, PLACE1002171, PLACE1002433, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002816, PLACE1002834, PLACE1003100, PLACE1003190, PLACE1003302, PLACE1003519, PLACE1003521, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885, PLACE1003923, PLACE1004302, PLACE1004471, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005287, PLACE1005876, PLACE1005966, PLACE1006167, PLACE1006438, PLACE1006482, PLACE1006829, PLACE1006878, PLACE1006917, PLACE1007014, PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008044, PLACE1008132, PLACE1008603, PLACE1009099, PLACE1009130, PLACE1009308, PLACE1009398, PLACE1010134, PLACE1010194, PLACE1010702, PLACE1010720, PLACE1010870, PLACE1011056, PLACE1011433, PLACE1011664, PLACE2000014, PLACE2000427, PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261, PLACE4000326, PLACE4000489, SKNMC1000011, THYRO1000085, THYRO1000242, THYRO1000585, THYRO1001100, THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000214, Y79AA1000231, Y79AA1000589, Y79AA1000752, Y79AA1001391, Y79AA1001613, Y79AA1001705, Y79AA1001963, Y79AA1002431, Y79AA1002472, Y79AA1002482,

[0069] The following 296 clones presumably belong to DNA- and/or RNA-binding proteins. HEMBA1000158, HEMBA1000216, HEMBA1000561, HEMBA1000591, HEMBA1000851, HEMBA1001088, HEMBA1001137, HEMBA1001405, HEMBA1001510, HEMBA1001804, HEMBA1001809, HEMBA1001819, HEMBA1001847, HEMBA1001869, HEMBA1002177, HEMBA1002935, HEMBA1003408, HEMBA1003545, HEMBA1003568, HEMBA1003591, HEMBA1003662, HEMBA1003684, HEMBA1003760, HEMBA1003783, HEMBA1003805, HEMBA1003953, HEMBA1004321, HEMBA1004354, HEMBA1004389, HEMBA1004479, HEMBA1004669, HEMBA1004847, HEMBA1004973, HEMBA1005202, HEMBA1005359, HEMBA1005931, HEMBA1006248, HEMBA1006278, HEMBA1006283, HEMBA1006359, HEMBA1006652, HEMBA1007087, HEMBA1007194, HEMBB1000264, HEMBB1000789, HEMBB1001011, HEMBB1001482, HEMBB1001736, HEMBB1001749, HEMBB1001839, HEMBB1002217, MAMMA1000183, MAMMA1000284, MAMMA1000731, MAMMA1001105, MAMMA1001222, MAMMA1001260, MAMMA1001743, MAMMA1001837, MAMMA1002385, MAMMA1002617, MAMMA1002869, MAMMA1002937, MAMMA1003011, NT2RM1000086, NT2RM1000539, NT2RM1000555, NT2RM1000666, NT2RM1000691, NT2RM1000826, NT2RM1000885, NT2RM1001059, NT2RM1001092, NT2RM2000371, NT2RM2000624, NT2RM2000735, NT2RM2001105, NT2RM2001424, NT2RM2001575, NT2RM2001605, NT2RM2001670, NT2RM2001771, NT2RM2001823, NT2RM2001989, NT2RM2002004, NT2RM2002014, NT2RM2002088, NT2RM2002091, NT2RM4000046, NT2RM4000104, NT2RM4000167, NT2RM4000191, NT2RM4000202, NT2RM4000531, NT2RM4000595, NT2RM4000733, NT2RM4000751, NT2RM4000996, NT2RM4001092, NT2RM4001140, NT2RM4001178, NT2RM4001200, NT2RM4001483, NT2RM4001592, NT2RM4001783, NT2RM4001823, NT2RM4001828, NT2RM4001858, NT2RM4001880, NT2RM4001979, NT2RM4002093, NT2RM4002109, NT2RP1000470, NT2RP1000493, NT2RP1000574, NT2RP1000902, NT2RP1000966, NT2RP1001013, NT2RP1001073, NT2RP1001080, NT2RP2000008, NT2RP2000153, NT2RP2000258, NT2RP2000297, NT2RP2001127, NT2RP2001174, NT2RP2001233, NT2RP2001511, NT2RP2001756, NT2RP2001869, NT2RP2002079, NT2RP2002099, NT2RP2002503, NT2RP2002591, NT2RP2002939, NT2RP2003157, NT2RP2003329, NT2RP2003347, NT2RP2003480, NT2RP2003522, NT2RP2003564, NT2RP2003714, NT2RP2004187, NT2RP2004568, NT2RP2004920, NT2RP2005003, NT2RP2005139, NT2RP2005168, NT2RP2005436, NT2RP2005496, NT2RP2005701, NT2RP2005763, NT2RP2005776, NT2RP2005942,

NT2RP2006043, NT2RP2006436, NT2RP2006464, NT2RP3000050, NT2RP3000512, NT2RP3000527, NT2RP3000562, NT2RP3000590, NT2RP3000603, NT2RP3000624, NT2RP3000632, NT2RP3000994, NT2RP3001057, NT2RP3001107, NT2RP3001120, NT2RP3001150, NT2RP3001155, NT2RP3001338, NT2RP3001398, NT2RP3001472, NT2RP3001672, NT2RP3001688, NT2RP3001724, NT2RP3001792, NT2RP3001855, NT2RP3002165, NT2RP3002399, NT2RP3002876, NT2RP3003138, NT2RP3003193, NT2RP3003251, NT2RP3003327, NT2RP3003555, NT2RP3004013, NT2RP3004078, NT2RP3004428, NT2RP3004490, NT2RP3004566, NT2RP3004594, NT2RP3004617, NT2RP3004618, NT2RP4000111, NT2RP4000398, NT2RP4000455, NT2RP4000518, NT2RP4000648, NT2RP4000865, NT2RP4000929, NT2RP4001080, NT2RP4001095, NT2RP4001213, NT2RP4001433, NT2RP4001568, NT2RP4001696, NT2RP4001753, NT2RP4001838, NT2RP4001938, NT2RP4002078, OVARC1000006, OVARC1000087, OVARC1000241, OVARC1000746, OVARC1000846, OVARC1001232, OVARC1001271, OVARC1001306, OVARC1001987, OVARC1002112, PLACE1000406, PLACE1000583, PLACE1000979, PLACE1001118, PLACE1001632, PLACE1001739, PLACE1002438, PLACE1002532, PLACE1002775, PLACE1002834, PLACE1003302, PLACE1003519, PLACE1003605, PLACE1003704, PLACE1003738, PLACE1003885, PLACE1004471, PLACE1004564, PLACE1004814, PLACE1005584, PLACE1005876, PLACE1005951, PLACE1006196, PLACE1006482, PLACE1006488, PLACE1006531, PLACE1006917, PLACE1007346, PLACE1007547, PLACE1007598, PLACE1007688, PLACE1007969, PLACE1008132, PLACE1009099, PLACE1009246, PLACE1009398, PLACE1009476, PLACE1009622, PLACE1010053, PLACE1010194, PLACE1010702, PLACE1010870, PLACE1011056, PLACE1011114, PLACE1011433, PLACE2000427, PLACE3000009, PLACE3000169, PLACE4000014, PLACE4000156, PLACE4000192, PLACE4000261, PLACE4000489, SKNMC1000091, THYRO 1000085, THYRO1000242, THYRO1000501, THYRO1001100, THYRO1001189, THYRO1001809, Y79AA1000037, Y79AA1000349, Y79AA1000752, Y79AA1001211, Y79AA1001312, Y79AA1001391, Y79AA1001613, Y79AA1002103, Y79AA1002472, Y79AA1002482, HEMBA1004596, OVARC1000148, PLACE1003334, THYRO1001661,

[0070] The following 66 clones presumably belong to the category of RNA synthesis-associated proteins.

HEMBA1000591, HEMBA1001579, HEMBA1003179, HEMBA1003591, HEMBA1006278, HEMBB1000226, NT2RM1000187, NT2RM1000852, NT2RM2000624, NT2RM2001989, NT2RM2002100, NT2RM4000191, NT2RM4001178, NT2RM4002093, NT2RP1000035, NT2RP1000272, NT2RP1000470, NT2RP1001080, NT2RP2000153, NT2RP2002928, NT2RP2003157, NT2RP2004568, NT2RP2005126, NT2RP2005436, NT2RP2005539, NT2RP2005605, NT2RP2005776, NT2RP2005942, NT2RP2006043, NT2RP2006238, NT2RP3000361, NT2RP3000397, NT2RP3001671, NT2RP3004504, NT2RP4000078, NT2RP4000111, NT2RP4000481, NT2RP4000518, NT2RP4000614, NT2RP4000929, NT2RP4001696, NT2RP4002058, OVARC1001232, OVARC1001577, PLACE1000406, PLACE1000596, PLACE1000755, PLACE1001739, PLACE1003704, PLACE1003885, PLACE1004564, PLACE1004814, PLACE1004902, PLACE1005373, PLACE1005646, PLACE1005876, PLACE1006196, PLACE1006626, PLACE1006878, PLACE1006917, PLACE1009476, PLACE1009925, PLACE1010194, PLACE1011114, THYRO1000121, Y79AA1001963,

[0071] The following 184 clones presumably belong to protein synthesis- and/or protein transport-associated proteins.

HEMBA1000012, HEMBA1000141, HEMBA1000592, HEMBA1003617, HEMBA1003773, HEMBA1004202, HEMBA1004276, HEMBA1004734, HEMBA1004847, HEMBA1004929, HEMBA1004930, HEMBA1005047, HEMBA1005202, HEMBA1006031, HEMBA1006272, HEMBA1006474, HEMBA1006652, HEMBA1006914, HEMBA1006973, HEMBA1007224, HEMBB1000915, HEMBB1001112, HEMBB1001137, HEMBB1001736, HEMBB1001831, HEMBB1001915, MAMMA1000085, MAMMA1000734, MAMMA1001008, MAMMA1002170, MAMMA1002219, MAMMA1002236, MAMMA1002619, NT2RM1000661, NT2RM1000833, NT2RM2000092, NT2RM2000504, NT2RM2000577, NT2RM2000821, NT2RM2001201, NT2RM2001592, NT2RM2001613, NT2RM2001648, NT2RM2001730, NT2RM2001760, NT2RM2002055, NT2RM4000155, NT2RM4000169, NT2RM4000344, NT2RM4000356, NT2RM4000421, NT2RM4000712, NT2RM4001054, NT2RM4001203, NT2RM4001382, NT2RM4001444, NT2RM4002062, NT2RM4002205, NT2RM4002623, NT2RP1000326, NT2RP1000522, NT2RP1000547, NT2RP1000746, NT2RP1000947, NT2RP1001569, NT2RP2000147, NT2RP2000710, NT2RP2000880, NT2RP2000943, NT2RP2001290, NT2RP2001392, NT2RP2001601, NT2RP2001613, NT2RP2001660, NT2RP2001740, NT2RP2002124, NT2RP2002606, NT2RP2002862, NT2RP2002959, NT2RP2002980, NT2RP2003137, NT2RP2003158, NT2RP2003391, NT2RP2003394, NT2RP2003401, NT2RP2003433, NT2RP2003704, NT2RP2003713, NT2RP2003737, NT2RP2003760, NT2RP2003981, NT2RP2004366, NT2RP2004389, NT2RP2004791, NT2RP2005012, NT2RP2005116, NT2RP2005360, NT2RP2005763, NT2RP2005784, NT2RP3000366, NT2RP3000759, NT2RP3000968, NT2RP3001113, NT2RP3001690, NT2RP3002045, NT2RP3002151, NT2RP3002529, NT2RP3002671, NT2RP3003301, NT2RP3003846, NT2RP3003876, NT2RP3004209, NT2RP4000370, NT2RP4000457, NT2RP4000879, NT2RP4000927, NT2RP4001041, NT2RP4001117,

NT2RP4001313, NT2RP4001315, NT2RP4001574, NT2RP4001592, OVARC1000013, OVARC1000071, OVARC1000085, OVARC1000465, OVARC1000564, OVARC1000771, OVARC1000862, OVARC1001171, OVARC1001180, OVARC1001342, PLACE1000007, PLACE1000061, PLACE1000081, PLACE1000492, PLACE1000863, PLACE1001092, PLACE1001748, PLACE1002090, PLACE1003174, PLACE1003915, PLACE1004104, PLACE1004270, PLACE1004743, PLACE1005557, PLACE1005813, PLACE1006170, PLACE1006488, PLACE1006829, PLACE1007706, PLACE1007729, PLACE1008273, PLACE1008402, PLACE1008790, PLACE1008813, PLACE1009094, PLACE1009130, PLACE1009477, PLACE1009721, PLACE1009845, PLACE1010074, PLACE1010547, PLACE1011109, PLACE1011229, PLACE1011477, PLACE1012031, PLACE2000404, PLACE3000059, PLACE3000121, PLACE4000269, PLACE4000654, SKNMC1000011, THYRO1000983, THYRO1001003, THYRO1001313, Y79AA1000560, Y79AA1000784, Y79AA1000968, Y79AA1001493, Y79AA1001875, Y79AA1002027, Y79AA1002209, HEMBA1006284,

[0072] The following 130 clones presumably belong to cytoskeleton-associated proteins.

HEMBA1000156, HEMBA1000168, HEMBA1000411, HEMBA1000588, HEMBA1001043, HEMBA1001651, HEMBA1001661, HEMBA1002102, HEMBA1002161, HEMBA1002939, HEMBA1003235, HEMBA1003581, HEMBA1004499, HEMBA1004534, HEMBA1004697, HEMBA1004929, HEMBA1004972, HEMBA1005582, HEMBA1005595, HEMBA1006344, HEMBA1006737, HEMBB1001175, HEMBB1001282, HEMBB1001562, HEMBB1001802, MAMMA1000824, MAMMA1001041, MAMMA1001576, MAMMA1001679, MAMMA1001735, MAMMA1002297, MAMMA1002351, MAMMA1002622, MAMMA1002637, MAMMA1003127, NT2RM1000850, NT2RM1000898, NT2RM2000030, NT2RM2000260, NT2RM2000691, NT2RM2001324, NT2RM4000169, NT2RM4000229, NT2RM4000515, NT2RM4001217, NT2RP1000202, NT2RP1000348, NT2RP1000460, NT2RP1000478, NT2RP1001033, NT2RP1001294, NT2RP1001302, NT2RP2000070, NT2RP2000812, NT2RP2000814, NT2RP2001168, NT2RP2001245, NT2RP2001634, NT2RP2001900, NT2RP2003307, NT2RP2003394, NT2RP2004041, NT2RP2004242, NT2RP2004538, NT2RP2004587, NT2RP2004681, NT2RP2004732, NT2RP2004978, NT2RP2005491, NT2RP2005531, NT2RP2005712, NT2RP2006275, NT2RP3000753, NT2RP3001113, NT2RP3001216, NT2RP3001239, NT2RP3001272, NT2RP3001554, NT2RP3001690, NT2RP3001799, NT2RP3002688, NT2RP3003061, NT2RP3003185, NT2RP3003230, NT2RP3004569, NT2RP3004578, NT2RP4001004, NT2RP4001086, NT2RP4001256, NT2RP4001567, NT2RP4001927, OVARC1000001, OVARC1000106, OVARC1000437, OVARC1000520, OVARC1000679, OVARC1001731, OVARC1002050, PLACE1001104, PLACE1002571, PLACE1002591, PLACE1002655, PLACE1002714, PLACE1003625, PLACE1005287, PLACE1006552, PLACE1007946, PLACE1008426, PLACE1010148, PLACE1010547, PLACE1010743, PLACE1010896, PLACE1010960, PLACE1011310, PLACE1011922, PLACE2000216, PLACE2000274, PLACE2000371, PLACE2000458, PLACE3000145, PLACE3000416, PLACE4000009, THYRO1000132, THYRO1001405, THYRO1001458, Y79AA1000368, Y79AA1000794, Y79AA1000833, Y79AA1000962, Y79AA1002208,

[0073] The following 54 clones presumably belong to cell division-associated and/or cell proliferation-associated proteins.

HEMBA1001019, HEMBA1001595, HEMBA1002363, HEMBA1002997, HEMBA1003136, HEMBA1003369, HEMBA1004131, HEMBA1004354, HEMBA1005621, HEMBB1000037, HEMBB1000264, MAMMA1001768, MAMMA1002769, NT2RM1000354, NT2RM1000430, NT2RM1000874, NT2RM2001256, NT2RM2001743, NT2RM2001896, NT2RM2002145, NT2RM4000215, NT2RM4001714, NT2RP1000163, NT2RP1000333, NT2RP1000439, NT2RP2000346, NT2RP2001397, NT2RP2002595, NT2RP2003177, NT2RP2003596, NT2RP2003912, NT2RP2004396, NT2RP2005037, NT2RP2005520, NT2RP2005669, NT2RP2005835, NT2RP3001730, NT2RP3002081, NT2RP4000210, NT2RP4000415, NT2RP4001414, NT2RP4001634, OVARC1000013, OVARC1000937, PLACE1001383, PLACE1002433, PLACE1004316, PLACE1005287, PLACE1008808, PLACE1010720, PLACE1010833, Y79AA1000748, Y79AA1001236, Y79AA1001394

[0074] The following 36 clones presumably belong to the category of embryogenesis- and/or development-associated proteins:

HEMBA1000518, HEMBA1001847, HEMBA1001869, HEMBA1003545, HEMBA1004973, HEMBB1002442, MAMMA1001837, NT2RM2001670, NT2RM4000046, NT2RM4000531, NT2RM4001140, NT2RM4001858, NT2RP2002078, NT2RP2004187, NT2RP2006436, NT2RP3000603, NT2RP3000994, NT2RP3001580, NT2RP3001708, NT2RP3003071, NT2RP3004472, NT2RP3004617, NT2RP4000246, NT2RP4001567, OVARC1000304, OVARC1000746, PLACE1000793, PLACE1002532, PLACE1003258, PLACE1003625, PLACE1004460, PLACE1009622, PLACE4000558, THYRO1000085, Y79AA1001391, Y79AA1001692

[0075] The following 30 clones presumably belong to cellular defense-associated proteins.

HEMBA1000005, HEMBA1000531, HEMBA1003417, HEMBA1006253, NT2RM4000354, NT2RM4001880, NT2RP1000333, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2000809, NT2RP2001536, NT2RP2002464, NT2RP2004920, NT2RP2005037, NT2RP3000590, NT2RP3001426, NT2RP3002062, NT2RP3002785, NT2RP3004262, NT2RP4001555, NT2RP4001638, PLACE1006958, PLACE1008275,

PLACE1009113, PLACE1011858, PLACE4000014, THYRO1000684, Y79AA1002139, Y79AA1002229

[0076] Although it is unclear whether or not 261 clones out of clones other than the above-mentioned clones belong to any of the above-described categories, these clones are predicted to have some functions, based on the homology search using their full-length sequences.

HEMBA1000030, HEMBA1000307, HEMBA1000333, HEMBA1000488, HEMBA1000523, HEMBA1001197, HEMBA1001302, HEMBA1001455, HEMBA1001675, HEMBA1001714, HEMBA1001744, HEMBA1001967, HEMBA1002151, HEMBA1002215, HEMBA1002458, HEMBA1002777, HEMBA1003098, HEMBA1003199, HEMBA1003615, HEMBA1003836, HEMBA1004295, HEMBA1004573, HEMBA1004604, HEMBA1004795, HEMBA1005101, HEMBA1005201, HEMBA1005206, HEMBA1005530, HEMBA1005666, HEMBA1005990, HEMBA1006268, HEMBA1006398, HEMBA1006445, HEMBA1007174, HEMBA1007251, HEMBB1000036, HEMBB1000144, HEMBB1000973, HEMBB1001058, HEMBB1001234, HEMBB1001288, HEMBB1001331, HEMBB1001384, HEMBB1002266, HEMBB1002510, HEMBB1002705, MAMMA1000055, MAMMA1000625, MAMMA1001075, MAMMA1001181, MAMMA1001259, MAMMA1001730, MAMMA1002143, MAMMA1002699, MAMMA1002972, MAMMA1003113, NT2RM1000118, NT2RM1000186, NT2RM1000244, NT2RM1000421, NT2RM1000499, NT2RM1000623, NT2RM1000883, NT2RM2000502, NT2RM2000599, NT2RM2000718, NT2RM2001065, NT2RM2001196, NT2RM2001983, NT2RM2002109, NT2RM2002142, NT2RM4000030, NT2RM4000139, NT2RM4000156, NT2RM4000386, NT2RM4000590, NT2RM4001047, NT2RM4001155, NT2RM4001256, NT2RM4001320, NT2RM4001340, NT2RM4001347, NT2RM4001371, NT2RM4001582, NT2RM4001611, NT2RM4001731, NT2RM4001969, NT2RM4002034, NT2RM4002075, NT2RM4002226, NT2RP1000040, NT2RP1000363, NT2RP1000481, NT2RP1000513, NT2RP1000733, NT2RP1000860, NT2RP1000954, NT2RP1001011, NT2RP1001395, NT2RP1001457, NT2RP1001494, NT2RP2000054, NT2RP2000067, NT2RP2000133, NT2RP2000157, NT2RP2000764, NT2RP2000965, NT2RP2001839, NT2RP2001883, NT2RP2001976, NT2RP2001985, NT2RP2002185, NT2RP2002442, NT2RP2002727, NT2RP2002741, NT2RP2002986, NT2RP2003121, NT2RP2003265, NT2RP2003272, NT2RP2003857, NT2RP2003871, NT2RP2004425, NT2RP2004476, NT2RP2004710, NT2RP2004816, NT2RP2005441, NT2RP2005490, NT2RP2005620, NT2RP2005654, NT2RP2005675, NT2RP2005753, NT2RP2005841, NT2RP2006598, NT2RP3000047, NT2RP3000233, NT2RP3000868, NT2RP3000869, NT2RP3001399, NT2RP3001407, NT2RP3001457, NT2RP3001587, NT2RP3001712, NT2RP3001819, NT2RP3001854, NT2RP3001931, NT2RP3002273, NT2RP3002631, NT2RP3002682, NT2RP3002770, NT2RP3002818, NT2RP3002948, NT2RP3002972, NT2RP3003032, NT2RP3003290, NT2RP3003411, NT2RP3003491, NT2RP3003500, NT2RP3003726, NT2RP3004348, NT2RP3004507, NT2RP4000129, NT2RP4000498, NT2RP4000528, NT2RP4000737, NT2RP4000979, NT2RP4001010, NT2RP4001207, NT2RP4001228, NT2RP4001260, NT2RP4001339, NT2RP4001351, NT2RP4001474, NT2RP4001966, NT2RP4002018, OVARC1000209, OVARC1000876, OVARC1001065, OVARC1001092, OVARC1001419, OVARC1001555, OVARC1001711, OVARC1001943, PLACE1000004, PLACE1000066, PLACE1000610, PLACE1000636, PLACE1000769, PLACE1000987, PLACE1001036, PLACE1001845, PLACE1001920, PLACE1002665, PLACE1003602, PLACE1003611, PLACE1004256, PLACE1004550, PLACE1004868, PLACE1004930, PLACE1005052, PLACE1005102, PLACE1005176, PLACE1005187, PLACE1005331, PLACE1005727, PLACE1006003, PLACE1006335, PLACE1006385, PLACE1006506, PLACE1007105, PLACE1007537, PLACE1007705, PLACE1007791, PLACE1007897, PLACE1008080, PLACE1008368, PLACE1008398, PLACE1008465, PLACE1008627, PLACE1009020, PLACE1009060, PLACE1009186, PLACE1009443, PLACE1009571, PLACE1009670, PLACE1010105, PLACE1010261, PLACE1010310, PLACE1010522, PLACE1010579, PLACE1010628, PLACE1010661, PLACE1010761, PLACE1011185, PLACE1011340, PLACE1011586, PLACE2000246, PLACE2000411, PLACE3000477, THYRO1000173, THYRO1000401, THYRO1000666, THYRO1001033, THYRO1001347, THYRO1001656, THYRO1001703, THYRO1001721, Y79AA1000059, Y79AA1000181, Y79AA1000268, Y79AA1000313, Y79AA1000540, Y79AA1000966, Y79AA1000985, Y79AA1001323, Y79AA1001402, Y79AA1001679, Y79AA1001923, Y79AA1002083, Y79AA1002307, Y79AA1002311, Y79AA1002487,

[0077] In some cases, the predicted functions based on the partial sequences are different from those based on the full-length sequences. The reason is that a protein does not always belong solely to a single category of the above-described functional categories, and therefore, a protein may belong to two or more of the predicted functional categories. Besides, additional functions can be found for the clones classified into these functional categories by further analyses.

[0078] Since the protein encoded by clones of the invention contains full-length amino acid sequence, it is possible to analyze its biological activity, and its effect on cellular conditions such as cell proliferation and differentiation by expressing the protein as a recombinant protein using an appropriate expression system, injecting the recombinant into the cell, or raising a specific antibody against the protein.

[0079] If the protein is a secretory protein, membrane protein, or protein associated with glycoprotein, signal trans-

duction, or transcription, its biological activity can be analyzed by the methods in "Gene Transcription" (Hames B.D., and Higgins S.J. edit, (1993)), "Glycobiology" (Fukuda M., and Kobata A. edit, (1993)), "Growth Factors" (McKay I., and Leigh I. edit, (1993)), "Extracellular Matrix" (Haralson M.A., and Hassell J.R. edit, (1995), "Transcription Factors" (Latchman D.S. edit, (1993)), "Signal Transduction" (Milligans G. edit, (1992)), "Protein Phosphorylation" (Hardies G. D. edit, (1993), and "Ion Channels" (Ashley R.H. edit, (1995) featured in "The Practical Approach Series" (IRL PRESS), or "Signal Transduction Protocols" (Kendall D.A., and Hill S.J. edit, (1995), "Glycoprotein Analysis in Biomedicine" (Hounsell E.F. edit, (1993)), featured in "Method in Molecular Biology" (Humana Press).

[0080] As to a protein associated with a disease, it is possible to perform a functional analysis as described above, but also possible to analyze correlation between the expression or the activity of the protein and a certain disease by using a specific antibody that is obtained by using expressed protein. Alternatively, it is possible to utilize the database Online Mendelian Inheritance in Man (OMIM) (http://www.ncbi.nlm.nih.gov/Omim/), which is a database of human genes and diseases, to analyze the protein.

New information is constantly being deposited in the OMIM database. Therefore, it is possible for one skilled in the art to find a new relationship between a particular disease and a gene of the present invention in the most up-to-date database.

[0081] Also, as for a secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., search of the OMIM with the following keywords resulted in the finding that the proteins are associated with many diseases (the result of the OMIM search for secrete and membrane proteins is shown below). Also, association between proteins associated to signal transduction or transcription and diseases is reported in "Transcription Factor Research-1999" (Fujii, Tamura, Kageyama, and Satake edit, (1999) Jikken-Igaku Zoukan, Vol.17, No.3), and "Gene Medicine" ((1999) Vol.3, No.2). For example, in tumors, many proteins have been shown to play a role, including secretory proteins, membrane proteins, and proteins associated with signal transduction, glycoprotein, and transcription, and also proteins associated with metabolism, cytoskeleton, and cell cycle, as described in "Tumor Biology" (Matsubara S. (1992) Syoukabou Life Science series). Thus, besides the proteins associated with diseases, many proteins described above are also potentially associated with diseases, and thus useful as a target in the medicinal industry.

[0082] The result of the OMIM search for secretory and membrane proteins is shown below, in which the keywords,

(1) secretion protein,
(2) membrane protein,
(3) channel, and
(4) extracellular matrix were used.

[0083] Shown in the search result are only the accession numbers in the OMIM. Using the number, data showing the relationship between a disease and a gene or protein can be seen. The OMIM data has been renewed everyday.

1) Secretion protein
268 entries found, searching for "secretion protein"
104760, 176860, 160900, 107400, 118910, 139320, 603850, 147572,176880, 600946, 603215, 157147, 600174, 151675, 170280, 179512, 179513,138120, 179509, 246700, 179510, 600626, 179511, 600998, 109270, 601489, 154545, 179490, 185860, 603216, 122559, 601746,147290, 602672, 146770, 603062, 179508, 131230, 601591, 602421, 139250, 167805, 167770, 600041, 600564, 118825, 601146, 300090, 600753, 601652, 600759, 600768, 602434, 182590, 603166, 308230, 602534, 603489, 107470, 150390, 104610, 173120, 158106, 143890, 306900, 308700, 134797, 137350, 227500, 176300, 107730, 600760, 138079, 120180, 120160, 120150, 124092, 138160, 101000, 227600, 600509, 601199, 142410, 104311, 193400, 201910, 107300, 122560, 272800, 217000, 590050, 147670, 133170, 176730, 300300, 134370, 274600, 120140,162151, 158070, 152790, 120120, 106100, 300200, 192340, 190160, 138040, 147470, 147620, 173350, 147380, 152200, 152760, 157145, 153450, 264080, 113811, 600937, 600840, 188545, 202110, 600514, 186590, 603372, 136435, 137241, 252800, 214500, 207750, 138850, 139191, 142640, 138130, 189907, 603692, 600633, 603355, 107270, 600377, 147892, 232200, 600281, 232800, 602358, 137035, 601771, 601769, 253200, 601933, 118444, 600270, 120700, 600945, 603732, 147660, 600761, 172400, 600823, 600877, 130080, 171060, 107740, 307800, 602843, 130660, 152780, 124020, 601124, 601340, 601604, 601610, 171050, 312060, 232700, 300159, 142703, 600734, 125255, 168450, 123812, 188540, 147940, 188450, 600839, 182452, 188400, 182280, 176760, 263200, 600264, 188826, 252650, 601185, 162641, 137216, 601398, 601538, 118888, 118445, 601745, 190180, 601922, 182098, 602008, 147440, 602384, 600031, 109160, 602663, 151670, 602682, 602730, 602779, 146880, 603061, 142704, 603140, 106150, 600732, 153620, 603318, 139392, 600042, 102200, 603493, 182100, 264300, 603795, 184600
2) Membrane protein
1017 entries found, searching for "membrane protein"

130500, 305360, 153330, 173610, 170995, 109270, 170993, 309060, 120920, 602333, 133740, 133710, 602690, 133730, 159430, 600897, 133090, 601178, 602413, 602003, 109280, 603237, 602173, 107776, 602334, 125305, 602335, 182879, 154045, 309845, 600594, 603718, 603241, 603214, 603657, 603177, 600182, 601476, 602879, 136950, 600723, 601114, 185880, 185881, 300096, 602257, 160900, 177070, 603062, 603344, 602977, 310200, 600959, 300100, 186945, 600039, 600267, 128240, 182900, 601097, 136430, 600946, 602534, 601047, 143450, 603141, 603700, 600579, 256540, 159440, 602414, 600403, 602048, 188860, 137290, 158343, 184756, 602910, 603179, 600279, 108733, 107770, 173335, 602625, 154050, 219800, 603850, 601028, 600447, 104225, 186946, 601767, 603143, 121015, 603215, 227400, 603735, 600179, 602421, 180721,
176801, 176860, 600753, 603142, 176790, 600266, 601239, 115501, 143890, 121014, 121011, 125950, 603534, 304040, 601134, 600754, 601510, 601595, 190315, 300172, 602216, 602261, 602262, 602461, 131560, 179514, 179512, 176981, 142461, 139310, 312080, 176640, 128239, 185470, 310300, 601403, 601757, 273800, 151460, 176943, 104311, 168468, 120130, 602887, 600164, 601531, 601832,104775, 600040, 603583, 176894, 602631, 166945, 182180, 120620, 141180, 601014, 139150, 182860, 177061, 600174, 180069, 191275, 104760, 601693, 300017, 603518, 601009, 134651, 601107, 603868, 600168, 136425, 603531, 603291, 600917, 603216, 102720, 300118, 179590, 135630, 602285, 107450, 602296, 303630, 176878, 120090, 600322, 138160, 601212, 603293, 131230, 112205, 600763, 600718, 300187, 170715, 601966, 300051, 602474,
120070, 600691, 600855, 182309, 602101, 602857, 194355, 162230, 600874, 113730, 155550, 602701, 306400, 601789, 231200, 107271, 175100, 182870, 305100, 301000, 601313, 157147, 147670, 139200, 603593,157655, 600934, 155970, 602049, 155960, 155760, 118990, 135620, 308230, 602694, 162060, 300023, 160993, 153619, 153432, 120131, 603823, 603167, 601023, 600816, 165040, 601681,166490, 300112, 120190, 300145, 163970, 600772, 602926, 602933, 602202, 400015, 151510, 600759, 602672, 602654, 603821, 116952, 151430, 602632, 155975, 602217, 150370, 600752, 601179, 600932, 603048, 603234, 601805, 603822, 603869, 601717, 601181, 313440, 139130, 107777, 109190, 603452, 191163, 191164, 602370, 176877, 103195, 600523, 191328, 601275, 204200, 602426, 603820, 600551, 600695, 600552, 600553, 602306, 601523,
602507, 602299, 600583, 114070, 600632, 603498, 185430, 600587, 235200, 173470, 603199, 601633, 602500, 208900, 180297, 156225, 516020, 190195, 141900, 102680, 193300, 101000, 193400, 300011, 107400, 257220,107741, 180380, 203200, 111700, 600024, 304800, 600065, 110750, 179605, 113705, 601638, 222900, 120120, 602509, 602469, 600930, 601383, 176261, 602574, 602997, 311770, 131550, 603616, 308700, 603372, 256100, 224100, 276903, 305900, 516000, 131195, 314555, 601567, 603866, 306900, 103390, 186720, 173850, 601050, 602505, 186590, 246530, 602689, 194380, 300041, 162643, 152790,120150, 600682, 600106, 272750, 188040, 602382, 601497, 113811, 182138, 212138, 601309, 109690, 114760, 176805, 601253, 123900, 602581, 189980,191190,110700, 600163, 137167, 600580, 601610, 190000, 123825, 603491,
600135, 186591, 173910, 138140, 107266, 120950, 601081, 603690, 244400, 312700, 171060, 601199, 601758, 170500, 277900, 601997, 314850, 601880, 603009, 120220, 603126, 164920, 602934, 164730, 163890, 603434, 107269, 602909, 600877, 256550, 164761, 602872, 120110, 126150, 158070, 266200, 223360, 250800, 269920, 252650, 603355, 154582, 138190, 300035, 602640, 227650, 158120, 153700, 182380, 155740, 204500, 603401, 601975, 300135, 136350, 602924, 300167, 185050, 176100, 300189, 151525, 300200, 165180, 230800, 602158, 602676, 603411, 193245, 120325, 601848, 192500, 603102, 147795, 245900, 137060, 147557,120650, 602377, 307800, 120930, 308100, 142800, 191092, 232300, 173510, 602225, 180470, 190930, 186357, 134638, 600544, 601373, 600509, 600359, 603784, 600395, 600653, 603754, 601597, 601066,
600185, 601295, 600978, 205400, 603274, 600418, 600839, 516050, 601691, 601007, 600650, 600308, 603261, 601193, 600004, 600017, 516040, 253800, 276901, 600019, 257200,108780, 300037, 300104, 300126, 255125, 203300, 300191, 426000, 302060, 304700, 201475, 252010, 193210, 311030, 306250, 248600, 191740, 108360, 131244, 600423, 232200, 191305, 231680, 103320, 190180, 600493, 111200, 226200, 312600, 600170, 111680, 186910, 203100, 600536, 600238,186830, 186760, 186745, 186711, 106180, 112203, 103180, 182530, 182160, 600644, 307030, 192321, 600667, 125647, 179080, 114207, 114860, 176000, 116930, 600748, 173515, 173325, 600377, 171760, 171050, 118425, 170260, 191315, 600798, 600821, 600823, 600444, 600840, 159465, 600857, 158380, 600867, 154360, 152427, 150330, 110900, 147840,147360, 147280,
146880, 312610, 120940, 142871, 142790, 600937, 142600,134390,111250, 600979, 600997, 142460, 186845, 134635, 601017, 139191, 139090, 138850, 601040, 138720, 122561, 131100, 123610, 217070, 100500, 603377, 602354, 603302, 603207, 603086, 602188, 602095, 603867, 603842, 603798, 602602, 601194, 602607, 603713, 603681, 601252, 603648, 603646, 603644, 601282, 601284, 603667, 603712, 603594, 601872, 603425, 601843, 603263, 603208, 601411, 603201, 603189, 601463, 603164, 603152, 603087, 602874, 601492, 602893, 602057, 602859, 602746, 603879, 603510, 602458, 603380, 601581, 603765, 603283, 601599, 601733, 601852, 602316, 601615, 601617, 602184, 602894, 603005, 603030, 603861, 602835, 602136, 600153, 600074, 600046, 600023, 601625, 516006, 600018, 600016, 516002, 601590, 313475, 313470, 600244,
600528, 601611, 600282, 600327, 601568, 600368, 601730, 601535, 601745, 601929, 300169, 300150, 300132, 601533, 600385, 600464, 600424, 600429, 601756, 601488, 516005, 251100, 516004, 600918, 516003, 602192,

516001, 240500, 600465, 602241, 602243, 230200, 601485, 601478, 601416, 602297, 601459, 601839, 602314, 193065, 193001, 191306, 600504, 601020, 191191, 602372, 190181, 600534, 188380, 186854, 186360, 600530, 185250, 182331, 600535, 182305, 601296, 600582, 600732, 600734, 600742, 600782, 176802, 176266, 600769, 601883, 600864, 601901, 176260, 173490, 600910, 601905, 171890, 600916, 601987, 602679, 162651, 161555, 160994, 602714, 602715, 602724, 602736, 300007, 602783, 275630, 602836, 270200, 602871, 159460, 602876, 154540, 153900, 602890, 601153, 602190, 602905, 153634, 153337, 602914,
152310, 151690, 151625, 602935, 602974, 150325, 602992, 150320, 250790, 603006, 603007, 603008, 150292, 233690, 603046, 150210, 603061, 147940, 603063, 221770, 223100, 603097, 147880, 603118, 147730, 146928, 146630, 142622, 603149, 603150, 603151, 600923, 138981, 138590, 138330, 216950, 603192, 138297, 603202, 601002, 602343, 138230, 136131, 603217, 603220, 134660, 131390, 131235, 603242, 603243, 130130, 602345, 126455, 601123, 126064, 125240, 602359, 603312, 602380, 603318, 123890, 123836, 603356, 603361, 603366, 123830, 179610, 188060, 123620, 120980, 186355, 118510, 114835, 114217, 113810, 603499, 182310, 111740, 109610, 603548, 603564, 108740, 603598, 603613, 107273, 603626, 602518, 179410, 603647, 602515, 603652, 106195, 602573, 178990, 105210, 104615, 167055, 603717, 104614, 603728,
104210, 603749, 603750, 103850, 602608, 603787, 603788, 603796, 173445, 103220, 102910, 102681, 102670, 102642, 603833, 173391, 102576,102575, 171833, 102573, 101800, 603875, 601108

3) Channel (member of membrane protein)

272 entries found, searching for "channel"

176266, 600724, 170500, 182390, 123825, 114208, 114205, 601784, 114206, 600937, 114204, 603415, 600053, 114209, 114207, 600760, 118425, 601011, 192500, 176261, 600761, 176260, 600359, 600228, 600877, 602235, 300008, 182389, 182391, 601328, 601534, 600504, 602323, 601958, 602780, 602781, 601327, 601012, 600734, 603208, 182392, 603220, 603219, 603888, 600054, 602232, 601745, 603537, 602604, 603796, 302910, 602866, 601013, 602905, 602906, 600163, 152427, 180901, 600702, 600308, 602754, 107776, 602024, 314555, 601949, 600235, 602023, 176263, 600681, 176265, 193245, 603305, 176258, 602983, 601219, 601141, 176267, 602343, 602726, 138253, 176262, 600003, 600397, 602872, 138249, 600843, 600935, 600580, 600845, 602158, 602106, 176264, 300110, 176257, 602717, 603493, 176268, 600932, 602727, 138254,
603652, 300138, 602420, 600570, 600150, 603583, 602345, 603749, 601142, 176256, 600846, 138252, 602982, 603787, 602836, 603788, 602566, 603651, 602421, 100690, 107777, 100725, 100710, 600509, 603061, 154275, 304040, 154276, 180902, 121014, 602368, 139311, 601383, 108745, 601313, 601042, 600131, 186360, 600109, 600229, 600170, 603319, 601485, 118503, 180903, 602076, 124030, 601059, 601212, 601218, 147450, 600855, 600919, 601154, 601157, 171060, 600968, 182139, 131230, 121015, 600421, 113730, 249210, 310500, 600637, 125950, 118800, 156490, 602974, 104610, 121011, 602522, 118504, 300041, 160900, 601382, 602103, 600465, 602014, 600442, 601109, 602481, 277900, 254210, 138247, 164920, 170280, 171050, 128100, 173910, 600884, 123885, 602887, 600232, 180297, 137192, 600304, 138251, 603053, 300103,
603152, 603199, 118511, 118508, 138079, 600983, 182307, 603324, 305990, 603418, 114080, 232200, 600046, 600040, 602403, 603750, 603785, 104210, 600019, 600300, 182860, 603852, 603853, 603855, 516060

4) Extracellular matrix

167 entries found, searching for "extracellular matrix"

603479, 602201, 601418, 601548, 154870, 115437, 602285, 602262, 602261,134797, 600754, 120361, 116935, 602263, 603320, 601807, 603321, 185250, 185261, 253700, 128239, 120324, 193300, 276901, 308700, 600514, 600261, 602109, 120140, 120150, 147557, 193400, 600536, 188826, 120180, 118661, 120320, 152200, 135821, 112260, 230740, 602090, 155760, 192975, 190182, 602108, 601463, 186745, 600900, 600985, 600758, 602369,179590, 601211, 600065, 602178, 600262, 182888, 182889, 151510, 182120, 150325, 190181, 150370, 186355, 193065, 165070, 154705, 147559, 146650, 146640, 153619, 175100, 187380, 231050, 188060, 135820, 156790, 130660, 301870, 128240, 600076, 600119, 193210, 600215, 600245, 121010, 150240, 600309, 600491, 222600, 120328, 600564, 600596, 600616, 600700, 600742, 120325, 138297, 600930,
156225, 601028, 601050, 601105, 253800, 601284, 601313, 120280, 310200, 601492, 120250, 601587, 601636, 601652, 601692, 601728, 120220, 601915, 602048, 155120, 310300, 120210, 120165, 120120, 118940, 116930, 602264, 116806, 602366, 120470, 602415, 602428, 602453, 602505, 602574, 603005, 603196, 603221, 603319, 107269, 216550, 103320, 603489, 603551, 603767, 603799, 603842

[0084] There are several methods for analyzing the expression levels of genes associated with diseases. Differences in gene expression levels between diseased and normal tissues are studied by the analytical methods, for example, Northern hybridization and differential display. Other examples include a method with high-density cDNA filter, a method with DNA microarray and methods with PCR amplification (Experimental Medicine, Vol.17, No. 8, 980-1056 (1999); Cell Engineering (additional volume) DNA Microarray and Advanced PCR Methods, Muramatsu & Naba (eds.), Shujunsya). The varying levels of gene expression between diseased tussues and normal tissues can be studied by any of these analytical methods. When explicit difference in the expression level is observed for a gene, it can be conclude that the gene is closely associated with a disease or disorder. Instead of diseased tissues, cultured cells can be used

for the assessment. Similarly, when gene expression is explicitly different between normal cells and cells reproducing disease-associated specific features, it can be concluded that the gene is closely associated with a disease or disorder. When the expression levels of genes are evidently varied during major cellular events (such as differentiation and apoptosis), the genes are involved in the cellular events and accordingly are candidates for disease- and/or disorder-associated genes. Further, genes exhibiting tissue-specific expression are genes playing important parts in the tissue functions and, therefore, can be candidates for genes associated with diseases and/or disorders affecting the tissues.

[0085] For example, non-enzymic protein glycation reaction is believed to be a cause for a variety of chronic diabetic complications. Accordingly, genes of which expression levels are elevated or decreased in a glycated protein-dependent manner in the endothelial cells, are associated with diabetic complications caused by glycated proteins (Diabetes 1996, 45 (Suppl. 3), S67-S72; Diabetes, 1997, 46 (Suppl. 2), S19-S25).

The onset of rheumatoid arthritis is thought to be involved in the proliferation of synovial cells covering inner surfaces of joint cavity and in inflammatory reaction resulted from the action of cytokines produced by leukocytes infiltrating into the joint synovial tissues (Rheumatism Information Center, http://www.rheuma-net.or.jp/). Recent studies have also revealed that tissue necrosis factor (TNF)-α participates in the onset (Current opinion in immunology 1999, 11, 657-662). When the expression of a gene exhibits responsiveness to the action of TNF on synovial cells, the gene is considered to be involved in rheumatoid arthritis. Many genes acting at the downstream of TNF-α and IL-1β among inflammation-associated cytokines have been previously identified. The respective stimulations are transduced through independent pathways of signaling cascade. There exists another signaling cascade for both stimulations, wherein NF-κ B is a common transducing molecule shared by the two stimulations (J. Leukoc. Biol., 1994, 56(5): 542-547). It has also been revealed that many inflammation-associated genes, including IL-2, IL-6 and G-CSF, are varied in the expression levels thereof in response to the signal through the common pathway (Trend Genet. 1999, 15(6): 229-235). It is assumed that genes of which expression levels are varied in response to the stimulation of TNF-α or IL-1β also participate in inflammation.

[0086] Ultraviolet radiation damage has been recognized as a risk factor for skin cancers, etc. (United States Environmental Protection Agency: Ozone Depletion Home Page, http://www.epa.gov/ozone/). Genes of which expression levels are varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with ultraviolet radiation damage of skin. In addition, genes associated with neural differentiation can be candidates for genes responsible for neurological diseases as well as candidates for genes usable for treating the diseases.

[0087] Clones exhibiting differences in the expression levels thereof can be selected by using gene expression analysis. The selection comprises, for example; analyzing cDNA clones by using high-density cDNA filter; and statistically treating the multiple signal values (signal values of radioisotope in the labeled probes or values obtained by measuring fluorescence intensities emitted from the fluorescent labels) for the respective clones by two-sample t-test, where the signal values are determined by multiple experiments of hybridization. The clones of interest are selectable based on the statistically significant differences in the signal distribution at $p<0.05$. However, selectable clones with significant difference in the expression levels thereof may be changed depending on the partial modification of statistical treatment. For example, the clones may be selected by conducting statistical treatment with two-sample t-test at $p<0.01$; or genes exhibiting more explicit differences in the expression levels thereof can be selected by performing statistical treatment with a pre-determined cut-off value for the significant signal difference. An alternative method is that the expression levels are simply compared with each other, and then, the clones of interest are selected based on the ratio of the expression levels thereof.

[0088] Clones that vary in their expression levels can also be selected by comparing the expression levels by PCR analysis, for example, by using the method of determining the band intensities representing the amounts of PCR products with ethidium bromide staining; the method of determining the values of radioisotope signals or fluorescence intensities of the PCR products when radiolabeled or fluorescent dye-labeled primers, respectively, are used in PCR amplification; or the method of determining the values of radioisotope signals or fluorescence intensities of the probes hybridized to the PCR products when radiolabeled or fluorescent dye-labeled probes, respectively, are used in the hybridization. If the expression level ratios obtained in multiple PCR experiments are constantly at least 2-fold, such a clone can be judged to vary in its expression level. When the ratios are several-fold or not less than 10-fold, the clone can be selected as a gene exhibiting the explicit difference in its expression level.

[0089] A survey of genes of which expression levels are varied specifically to the glycated protein in the endothelial cells has revealed genes with elevated expression levels, HEMBA1003958, HEMBA1004850, MAMMA1001256, MAMMA1002132, PLACE2000411 and PLACE3000119. On the other hand, a gene of which expression level is decreased specifically to the glycated protein is MAMMA1001783. These clones are genes associated with diabetes.

[0090] A survey of genes of which expression levels are varied in response to TNF-α (Tumor Necrosis Factor-alpha) in the primary cell culture of synovial tissue has revealed the following clones with elevated expression levels in the presence of TNF-α:

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000046, HEMBA1000076, HEMBA1000111, HEMBA1000168, HEMBA1000185, HEMBA1000201, HEMBA1000231, HEMBA1000243, HEMBA1000280,

HEMBA1000282, HEMBA1000304, HEMBA1000307, HEMBA1000327, HEMBA1000356, HEMBA1000376,
HEMBA1000387, HEMBA1000390, HEMBA1000418, HEMBA1000460, HEMBA1000491, HEMBA1000501,
HEMBA1000518, HEMBA1000519, HEMBA1000520, HEMBA1000531, HEMBA1000534, HEMBA1000542,
HEMBA1000545, HEMBA1000591, HEMBA1000592, HEMBA1000594, HEMBA1000636, HEMBA1000655,
HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000722, HEMBA1000726,
HEMBA1000827, HEMBA1000870, HEMBA1000918, HEMBA1000971, HEMBA1000974, HEMBA1000986,
HEMBA1001019, HEMBA1001043, HEMBA1001051, HEMBA1001059, HEMBA1001060, HEMBA1001071,
HEMBA1001080, HEMBA1001109, HEMBA1001140, HEMBA1001172, HEMBA1001196, HEMBA1001213,
HEMBA1001226, HEMBA1001281, HEMBA1001299, HEMBA1001302, HEMBA1001303, HEMBA1001323,
HEMBA1001326, HEMBA1001327, HEMBA1001330, HEMBA1001351, HEMBA1001407, HEMBA1001411,
HEMBA1001446, HEMBA1001454, HEMBA1001569, HEMBA1001647, HEMBA1001714, HEMBA1001800,
HEMBA1001804, HEMBA1001809, HEMBA1001888, HEMBA1001912, HEMBA1001921, HEMBA1001967,
HEMBA1002084, HEMBA1002161, HEMBA1002166, HEMBA1002241, HEMBA1002337, HEMBA1002363,
HEMBA1002389, HEMBA1002458, HEMBA1002460, HEMBA1002469, HEMBA1002538, HEMBA1002542,
HEMBA1002547, HEMBA1002609, HEMBA1002624,
HEMBA1002659, HEMBA1002750, HEMBA1002770, HEMBA1002779, HEMBA1002810, HEMBA1002816,
HEMBA1002818, HEMBA1002850, HEMBA1002863, HEMBA1003021, HEMBA1003033, HEMBA1003078,
HEMBA1003166, HEMBA1003202, HEMBA1003204, HEMBA1003229, HEMBA1003235, HEMBA1003276,
HEMBA1003286, HEMBA1003296, HEMBA1003370, HEMBA1003376, HEMBA1003403, HEMBA1003418,
HEMBA1003433, HEMBA1003447, HEMBA1003560, HEMBA1003569, HEMBA1003571, HEMBA1003591,
HEMBA1003597, HEMBA1003598, HEMBA1003621, HEMBA1003656, HEMBA1003662, HEMBA1003680,
HEMBA1003715, HEMBA1003725, HEMBA1003729, HEMBA1003733, HEMBA1003742, HEMBA1003773,
HEMBA1003783, HEMBA1003950, HEMBA1004012, HEMBA1004015, HEMBA1004048, HEMBA1004074,
HEMBA1004086, HEMBA1004111, HEMBA1004131, HEMBA1004202, HEMBA1004203, HEMBA1004207,
HEMBA1004248, HEMBA1004274, HEMBA1004321, HEMBA1004330, HEMBA1004356, HEMBA1004366,
HEMBA1004405, HEMBA1004408, HEMBA1004429, HEMBA1004499, HEMBA1004507, HEMBA1004509,
HEMBA1004542, HEMBA1004596, HEMBA1004604, HEMBA1004776, HEMBA1004889, HEMBA1004934,
HEMBA1004978, HEMBA1005019, HEMBA1005047, HEMBA1005206, HEMBA1005219, HEMBA1005274,
HEMBA1005331, HEMBA1005338, HEMBA1005394, HEMBA1005423, HEMBA1005576, HEMBA1005732,
HEMBA1005746, HEMBA1006091, HEMBA1006142, HEMBA1006173, HEMBA1006198, HEMBA1006253,
HEMBA1006268, HEMBA1006309, HEMBA1006377, HEMBA1006474, HEMBA1006486, HEMBA1006492,
HEMBA1006502, HEMBA1006535, HEMBA1006579, HEMBA1006648, HEMBA1006659, HEMBA1006885,
HEMBA1006929, HEMBA1006941, HEMBA1007078, HEMBA1007080, HEMBA1007121, HEMBA1007194,
HEMBA1007300, HEMBA1007301, HEMBA1007322, HEMBB1000036, HEMBB1000044, HEMBB1000089,
HEMBB1000215, HEMBB1000217, HEMBB1000272, HEMBB1000420, HEMBB1000591, HEMBB1000593,
HEMBB1000631, HEMBB1000835, HEMBB1000887, HEMBB1000908, HEMBB1000975, HEMBB1000985,
HEMBB1001011, HEMBB1001014, HEMBB1001112, HEMBB1001133, HEMBB1001331, HEMBB1001337,
HEMBB1001366, HEMBB1001367, HEMBB1001384, HEMBB1001394, HEMBB1001429, HEMBB1001463,
HEMBB1001619, HEMBB1001684, HEMBB1001706, HEMBB1001753, HEMBB1001797, HEMBB1001802,
HEMBB1001812, HEMBB1001874, HEMBB1001910, HEMBB1001915, HEMBB1001973, HEMBB1001983,
HEMBB1001990, HEMBB1002190, HEMBB1002193, HEMBB1002249, HEMBB1002329, HEMBB1002342,
HEMBB1002371, HEMBB1002409, HEMBB1002442, HEMBB1002489, HEMBB1002492, HEMBB1002520,
HEMBB1002534, HEMBB1002596, HEMBB1002664, HEMBB1002692, HEMBB1002697, HEMBB1002705,
MAMMA1000092, MAMMA1000155, MAMMA1000163, MAMMA1000173, MAMMA1000175, MAMMA1000227,
MAMMA1000241, MAMMA1000257, MAMMA1000264, MAMMA1000266, MAMMA1000270, MAMMA1000307,
MAMMA1000410, MAMMA1000413, MAMMA1000416, MAMMA1000421, MAMMA1000472, MAMMA1000501,
MAMMA1000605, MAMMA1000643, MAMMA1000670, MAMMA1000684, MAMMA1000696, MAMMA1000732,
MAMMA1000752, MAMMA1000802, MAMMA1000824, MAMMA1000905, MAMMA1000921, MAMMA1000931,
MAMMA1000957, MAMMA1000962,
MAMMA1000998, MAMMA1001008, MAMMA1001050, MAMMA1001074, MAMMA1001078, MAMMA1001292,
MAMMA1001397, MAMMA1001476, MAMMA1001743, MAMMA1001744, MAMMA1001754, MAMMA1001760,
MAMMA1001785, MAMMA1001858, MAMMA1001908, MAMMA1002236, MAMMA1002267, MAMMA1002292,
MAMMA1002311, MAMMA1002322, MAMMA1002359, MAMMA1002362, MAMMA1002485, MAMMA1002494,
MAMMA1002597, MAMMA1002598, MAMMA1002665, MAMMA1002671, MAMMA1002684, MAMMA1002748,
MAMMA1002775, MAMMA1002830, MAMMA1002858, MAMMA1002868, MAMMA1002886, MAMMA1002887,
MAMMA1002892, MAMMA1002909, MAMMA1002937, MAMMA1002947, MAMMA1002964, MAMMA1002970,
MAMMA1003013, MAMMA1003150, NT2RM1000039, NT2RM1000062, NT2RM1000080, NT2RM1000086,
NT2RM1000127, NT2RM1000132, NT2RM1000187, NT2RM1000199, NT2RM1000244, NT2RM1000256,

NT2RM1000272, NT2RM1000318, NT2RM1000354, NT2RM1000377, NT2RM1000430, NT2RM1000499, NT2RM1000539, NT2RM1000553, NT2RM1000563, NT2RM1000699, NT2RM1000742, NT2RM1000826, NT2RM1000829, NT2RM1000833, NT2RM1000882, NT2RM1000898, NT2RM1000905, NT2RM1001092, NT2RM2000013, NT2RM2000032, NT2RM2000042, NT2RM2000101, NT2RM2000124, NT2RM2000192, NT2RM2000259, NT2RM2000260, NT2RM2000363, NT2RM2000368, NT2RM2000402, NT2RM2000452, NT2RM2000952, NT2RM2001221, NT2RM2002014, NT2RM2002030, NT2RM4000156, NT2RM4000349, NT2RM4000395, NT2RM4000457, NT2RM4000511, NT2RM4000514, NT2RM4000698, NT2RM4000764, NT2RM4001016, NT2RM4001084, NT2RM4001594, NT2RM4001629, NT2RM4001662, NT2RM4001841, NT2RM4002093, NT2RM4002109, NT2RM4002145, NT2RM4002189, NT2RM4002194, NT2RM4002226, NT2RP1000170, NT2RP1000439, NT2RP1000478, NT2RP1000513, NT2RP1000701, NT2RP1000856, NT2RP1001361, NT2RP2000097, NT2RP2000239, NT2RP2000288, NT2RP2000328, NT2RP2000329, NT2RP2000369, NT2RP2000422, NT2RP2000842, NT2RP2000965, NT2RP2001245, NT2RP2001440, NT2RP2001560, NT2RP2001634, NT2RP2001663, NT2RP2001677, NT2RP2001762, NT2RP2002270, NT2RP2002312, NT2RP2002316, NT2RP2002333, NT2RP2002706, NT2RP2002925, NT2RP2002959, NT2RP2002987, NT2RP2003125, NT2RP2003137, NT2RP2003237, NT2RP2003272, NT2RP2003596, NT2RP2003604, NT2RP2003643, NT2RP2003968, NT2RP2003976, NT2RP2004194, NT2RP2004321, NT2RP2005037, NT2RP2005140, NT2RP2005204, NT2RP2005293, NT2RP2005457, NT2RP2005555, NT2RP2005600, NT2RP2005701, NT2RP2005719, NT2RP2005722, NT2RP2005773, NT2RP2005890, NT2RP2006023, NT2RP2006071, NT2RP3000186, NT2RP3000341, NT2RP3000599, NT2RP3000632, NT2RP3000644, NT2RP3000852, NT2RP3000968, NT2RP3001096, NT2RP3001109, NT2RP3001126, NT2RP3001147, NT2RP3001449, NT2RP3001529, NT2RP3001753, NT2RP3001854, NT2RP3001915, NT2RP3001969, NT2RP3002081, NT2RP3002142, NT2RP3002399, NT2RP3002590, NT2RP3002603, NT2RP3002810, NT2RP3002876, NT2RP3003311, NT2RP3003330, NT2RP3003672, NT2RP3004209, NT2RP3004378, NT2RP4000078, NT2RP4000541, NT2RP4000588, NT2RP4001219, NT2RP4001228, NT2RP4001276, NT2RP4001507, NT2RP4002047, NT2RP5003459, NT2RP5003492, OVARC1000085, OVARC1000087, OVARC1000106, OVARC1000151, OVARC1000198, OVARC1000431, OVARC1000440, OVARC1000564, OVARC1000605, OVARC1000679, OVARC1000883, OVARC1000912, OVARC1000960, OVARC1000971, OVARC1001038, OVARC1001055, OVARC1001085, OVARC1001129, OVARC1001167, OVARC1001339, OVARC1001425, OVARC1001745, OVARC1001762, OVARC1001766, OVARC1001942, OVARC1002044, OVARC1002138, PLACE1000004, PLACE1000005, PLACE1000420, PLACE1000547, PLACE1000562, PLACE1000653, PLACE1001168, PLACE1001311, PLACE1001377, PLACE1001920, PLACE1001983, PLACE1002066, PLACE1002072, PLACE1002140, PLACE1002171, PLACE1002319, PLACE1002474, PLACE1002499, PLACE1002532, PLACE1002665, PLACE1003025, PLACE1003145, PLACE1003361, PLACE1003605, PLACE1003704, PLACE1003783, PLACE1003885, PLACE1004405, PLACE1004629, PLACE1004686, PLACE1004930, PLACE1005066, PLACE1005077, PLACE1005630, PLACE1005876, PLACE1006143, PLACE1006325, PLACE1006488, PLACE1006805, PLACE1006829, PLACE1007286, PLACE1007858, PLACE1008201, PLACE1009045, PLACE1009113, PLACE1009621, PLACE1010106, PLACE1010310, PLACE1010622, PLACE1010944, PLACE1010965, PLACE1011185, PLACE1011332, PLACE1011635, PLACE1011646, PLACE1011725, PLACE2000014, PLACE2000264, PLACE2000394, PLACE2000419, PLACE3000160, PLACE3000220, PLACE3000254, PLACE3000271, PLACE3000339, PLACE3000341, PLACE3000350, PLACE3000353, PLACE3000401, PLACE4000300, SKNMC1000091, THYRO1000855, THYRO1001559, Y79AA1000065, Y79AA1000202, Y79AA1000214, Y79AA1000346, Y79AA1000784, Y79AA1000833, Y79AA1000968, Y79AA1001555, Y79AA1002220

[0091] On the other hand, clones with decreased expression levels in the presence of TNFα are:

HEMBA1002150, HEMBB1000240, NT2RM2000469, NT2RM2000984, NT2RM2001688, NT2RM4000290, NT2RM4000496, NT2RM4000590, NT2RM4001047, NT2RM4001582, NT2RM4001611, NT2RM4001650, NT2RM4002075, NT2RM4002128, NT2RP1000174, NT2RP1000243, NT2RP1000581, NT2RP1000688, NT2RP1000767, NT2RP1000825, NT2RP1001185; NT2RP1001286, NT2RP1001432, NT2RP1001457, NT2RP2000001, NT2RP2000248, NT2RP2000841, NT2RP2001813, NT2RP2002137, NT2RP2002928, NT2RP2003517, NT2RP2003559, NT2RP2003564, NT2RP2004933, NT2RP2005038, NT2RP2006365, NT2RP3000072, NT2RP3000320, NT2RP3000484, NT2RP3000980, NT2RP3001111, NT2RP3001420, NT2RP3001495, NT2RP3002056, NT2RP3002057, NT2RP3002545, NT2RP3002713, NT2RP3002799, NT2RP3002869, NT2RP3002953, NT2RP3002955, NT2RP3003282, NT2RP3003290, NT2RP3003384, NT2RP3003385, NT2RP3003870, NT2RP3004207, NT2RP3004262, NT2RP3004527, NT2RP4000500, NT2RP4000524, NT2RP4000787, NT2RP4000927, NT2RP4000955, NT2RP4000989, NT2RP4001442, NT2RP4001638, NT2RP4001950, NT2RP4002888, NT2RP5003524, OVARC1001270, PLACE1000246, PLACE1002816.

[0092] These are rheumatoid arthritis-associated clones.

[0093] A survey of genes of which expression levels are varied in primary cultured skin fibroblast cells exposed to ultraviolet light has revealed the following clones with elevated expression levels by ultraviolet radiation: HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100, NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC 1000004, OVARC1001092, OVARC1001342, PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196, NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070, THYRO1001100, Y79AA1000342

[0094] On the other hand, the expression levels of the following clones were decreased by ultraviolet radiation: HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231, HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390, HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490, HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870, HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265, HEMBA1001281, HEMBA1001289, HEMBA1001299, HEMBA1001303, HEMBA1001310, HEMBA1001323, HEMBA1001595, HEMBA1001620, HEMBA1001640, HEMBA1001678, HEMBA1001712, HEMBA1001835, HEMBA1001950, HEMBA1001987, HEMBA1002253, HEMBA1002321, HEMBA1002341, HEMBA1002419, HEMBA1002679, HEMBA1002728, HEMBA1002818, HEMBA1002935, HEMBA1002999, HEMBA1003034, HEMBA1003071, HEMBA1003098, HEMBA1003142, HEMBA1003175, HEMBA1003202, HEMBA1003212, HEMBA1003220, HEMBA1003276, HEMBA1003373, HEMBA1003417, HEMBA1003447, HEMBA1003528, HEMBA1003684, HEMBA1003799, HEMBA1003885, HEMBA1003989, HEMBA1004011, HEMBA1004055, HEMBA1004133, HEMBA1004225, HEMBA1004272, HEMBA1004353, HEMBA1004631, HEMBA1004669, HEMBA1004705, HEMBA1004753, HEMBA1004776, HEMBA1004803, HEMBA1004816, HEMBA1004900, HEMBA1005047, HEMBA1005079, HEMBA1005101, HEMBA1005149, HEMBA1005152, HEMBA1005202, HEMBA1005314, HEMBA1005372, HEMBA1005511, HEMBA1005513, HEMBA1005518, HEMBA1005570, HEMBA1005577, HEMBA1005581, HEMBA1005588, HEMBA1005609, HEMBA1005632, HEMBA1005853, HEMBA1006031, HEMBA1006035, HEMBA1006485, HEMBA1006486, HEMBA1006502, HEMBA1006696, HEMBA1006789, HEMBA1006796, HEMBA1007085, HEMBA1007224, HEMBA1007301, HEMBA1007319, HEMBA1007341, HEMBA1007342, HEMBB1000036, HEMBB1000037, HEMBB1000217, HEMBB1000266, HEMBB1000317, HEMBB1000336, HEMBB1000354, HEMBB1000369, HEMBB1000399, HEMBB1000434, HEMBB1000438, HEMBB1000592, HEMBB1000673, HEMBB1000789, HEMBB1000810, HEMBB1000883, HEMBB1000887, HEMBB1001105, HEMBB1001182, HEMBB1001242, HEMBB1001267, HEMBB1001424, HEMBB1001464, HEMBB1001531, HEMBB1001618, HEMBB1001996, HEMBB1002092, HEMBB1002139, HEMBB1002142, HEMBB1002190, HEMBB1002453, HEMBB1002520, HEMBB1002550, HEMBB1002556, HEMBB1002600, HEMBB1002664, MAMMA1000009, MAMMA1000055, MAMMA1000069, MAMMA1000133, MAMMA1000171, MAMMA1000173, MAMMA1000287, MAMMA1000416, MAMMA1000585, MAMMA1000713, MAMMA1000760, MAMMA1000798, MAMMA1000831, MAMMA1000875, MAMMA1000876, MAMMA1000877, MAMMA1000906, MAMMA1000931, MAMMA1000962, MAMMA1001133, MAMMA1001139, MAMMA1001243, MAMMA1001271, MAMMA1001274, MAMMA1001298, MAMMA1001606, MAMMA1001630, MAMMA1001670, MAMMA1001743, MAMMA1001751, MAMMA1002140, MAMMA1002145, MAMMA1002158, MAMMA1002170, MAMMA1002236, MAMMA1002311, MAMMA1002498, MAMMA1002754, MAMMA1002780, MAMMA1002820, MAMMA1002843, MAMMA1002844, MAMMA1002871, MAMMA1003047, NT2RM1000037, NT2RM1000039, NT2RM1000080, NT2RM1000086, NT2RM1000341, NT2RM1000499, NT2RM1000669, NT2RM1000746, NT2RM1000781, NT2RM1000885, NT2RM1000905, NT2RM1000962, NT2RM2000239, NT2RM2000260, NT2RM2000371, NT2RM2000639, NT2RM2000649, NT2RM2000735, NT2RM2000821, NT2RM2000984, NT2RM2001035, NT2RM2001065, NT2RM2001105, NT2RM2001177, NT2RM2001194, NT2RM2001196, NT2RM2001243, NT2RM2001256, NT2RM2001424, NT2RM2001588, NT2RM2001635, NT2RM2001648, NT2RM2001652, NT2RM2001668, NT2RM2001706, NT2RM2001727, NT2RM2001730, NT2RM2001743, NT2RM2001753, NT2RM2001760, NT2RM2001771, NT2RM2001785, NT2RM2001800, NT2RM2001855, NT2RM2001896, NT2RM2001997, NT2RM2002030, NT2RM2002049, NT2RM2002091, NT2RM2002142, NT2RM2002145, NT2RM2002178, NT2RM2002580, NT2RM4000215, NT2RM4000344, NT2RM4000368, NT2RM4000421, NT2RM4000425, NT2RM4000457, NT2RM4000496, NT2RM4000515, NT2RM4000712, NT2RM4000787, NT2RM4000813, NT2RM4000820, NT2RM4000852, NT2RM4000950, NT2RM4000996, NT2RM4001016, NT2RM4001047, NT2RM4001054, NT2RM4001140, NT2RM4001151, NT2RM4001187, NT2RM4001204, NT2RM4001258, NT2RM4001437, NT2RM4001454, NT2RM4001489, NT2RM4001605, NT2RM4001611, NT2RM4001666, NT2RM4001710, NT2RM4001714, NT2RM4001715, NT2RM4001731, NT2RM4001741, NT2RM4001746, NT2RM4001856, NT2RM4001938, NT2RM4001940, NT2RM4001984,

NT2RP4000449, NT2RP4000515, NT2RP4000519, NT2RP4000528, NT2RP4000556, NT2RP4000588,
NT2RP4000638, NT2RP4000648, NT2RP4000973, NT2RP4000996, NT2RP4001006, NT2RP4001029,
NT2RP4001041, NT2RP4001100, NT2RP4001117, NT2RP4001174, NT2RP4001235, NT2RP4001274,
NT2RP4001276, NT2RP4001315, NT2RP4001373, NT2RP4001389, NT2RP4001433, NT2RP4001502,
NT2RP4001524, NT2RP4001567, NT2RP4001574, NT2RP4001677, NT2RP4001753, NT2RP4001927,
NT2RP4002052, NT2RP4002058, NT2RP4002071, NT2RP4002078, NT2RP4002083, NT2RP5003461,
NT2RP5003512, NT2RP5003522, OVARC1000085, OVARC1000091, OVARC1000106, OVARC1000109,
OVARC1000114, OVARC1000148, OVARC1000168, OVARC1000198, OVARC1000240, OVARC1000241,
OVARC1000288, OVARC1000302, OVARC1000309, OVARC1000326, OVARC1000335, OVARC1000347,
OVARC1000384, OVARC1000411, OVARC1000414, OVARC1000420, OVARC1000431, OVARC1000437,
OVARC1000440, OVARC1000442, OVARC1000465, OVARC1000473, OVARC1000479, OVARC1000486,
OVARC1000526, OVARC1000556, OVARC1000557, OVARC1000564, OVARC1000573, OVARC1000578,
OVARC1000588, OVARC1000605, OVARC1000622, OVARC1000678, OVARC1000679, OVARC1000681,
OVARC1000703, OVARC1000730, OVARC1000746, OVARC1000769, OVARC1000781, OVARC1000787,
OVARC1000800, OVARC1000834, OVARC1000846, OVARC1000850, OVARC1000862, OVARC1000876,
OVARC1000883, OVARC1000891, OVARC1000897, OVARC1000912, OVARC1000915, OVARC1000924,
OVARC1000937, OVARC1000945, OVARC1000948, OVARC1000959, OVARC1000960, OVARC1000984,
OVARC1000996, OVARC1000999, OVARC1001000, OVARC1001010, OVARC1001011, OVARC1001032,
OVARC1001034, OVARC1001038, OVARC1001040, OVARC1001044, OVARC1001055, OVARC1001062,
OVARC1001085, OVARC1001117, OVARC1001118, OVARC1001162, OVARC1001167, OVARC1001170,
OVARC1001173, OVARC1001180, OVARC1001232, OVARC1001240, OVARC1001261, OVARC1001268,
OVARC1001270, OVARC1001271, OVARC1001282, OVARC1001296, OVARC1001306, OVARC1001329,
OVARC1001330, OVARC1001339, OVARC1001341, OVARC1001344, OVARC1001360, OVARC1001369,
OVARC1001376, OVARC1001381, OVARC1001399, OVARC1001417, OVARC1001419, OVARC1001436,
OVARC1001496, OVARC1001506, OVARC1001525, OVARC1001542, OVARC1001600, OVARC1001668,
OVARC1001702, OVARC1001731, OVARC1001745, OVARC1001762, OVARC1001791, OVARC1001802,
OVARC1001812, OVARC1001813, OVARC1001820, OVARC1001861, OVARC1001873, OVARC1001879,
OVARC1001880, OVARC1001883, OVARC1001900, OVARC1001911, OVARC1001916, OVARC1001928,
OVARC1001942, OVARC1001949, OVARC1001950, OVARC1001987, OVARC1001989, OVARC1002044,
OVARC1002050, OVARC1002066, OVARC1002107, OVARC1002112, OVARC1002127, OVARC1002165,
PLACE1000004, PLACE1000078, PLACE1000081, PLACE1000142, PLACE1000184, PLACE1000185,
PLACE1000246, PLACE1000292, PLACE1000332, PLACE1000383, PLACE1000401, PLACE1000406,
PLACE1000420, PLACE1000421, PLACE1000435, PLACE1000453, PLACE1000481, PLACE1000562,
PLACE1000583, PLACE1000610, PLACE1000656, PLACE1000785, PLACE1000798, PLACE1000909,
PLACE1000948, PLACE1001010, PLACE1001076, PLACE1001092, PLACE1001104, PLACE1001171,
PLACE1001185, PLACE1001279, PLACE1001304, PLACE1001311, PLACE1001323, PLACE1001351,
PLACE1001366, PLACE1001502, PLACE1001534, PLACE1001602, PLACE1001603, PLACE1001608,
PLACE1001610, PLACE1001632, PLACE1001634, PLACE1001720, PLACE1001729, PLACE1001739,
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PLACE1001912, PLACE1001928, PLACE1001989, PLACE1002072, PLACE1002090, PLACE1002115,
PLACE1002150, PLACE1002170, PLACE1002319, PLACE1002342, PLACE1002395, PLACE1002399,
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PLACE1002583, PLACE1002685, PLACE1002768, PLACE1002772, PLACE1002782, PLACE1002794,
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PLACE1003176, PLACE1003190, PLACE1003200, PLACE1003205, PLACE1003238, PLACE1003249,
PLACE1003302, PLACE1003353, PLACE1003373, PLACE1003383, PLACE1003516, PLACE1003521,
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PLACE1003784, PLACE1003833, PLACE1003870, PLACE1003886, PLACE1003888, PLACE1003903,
PLACE1003936, PLACE1003968, PLACE1004103, PLACE1004114, PLACE1004118, PLACE1004242,
PLACE1004256, PLACE1004284, PLACE1004289, PLACE1004316, PLACE1004336, PLACE1004384,
PLACE1004388, PLACE1004405, PLACE1004425, PLACE1004428, PLACE1004451, PLACE1004467,
PLACE1004491, PLACE1004510, PLACE1004548, PLACE1004658, PLACE1004672, PLACE1004693,
PLACE1004716, PLACE1004777, PLACE1004813, PLACE1004824, PLACE1004827, PLACE1004836,
PLACE1004840, PLACE1004885, PLACE1004913, PLACE1004918, PLACE1004930, PLACE1004934,
PLACE1004972, PLACE1004982, PLACE1004985, PLACE1005026, PLACE1005101, PLACE1005102,
PLACE1005128, PLACE1005176, PLACE1005181, PLACE1005187, PLACE1005232, PLACE1005261,
PLACE1005277, PLACE1005287, PLACE1005305, PLACE1005327, PLACE1005331, PLACE1005373,

PLACE1005884, PLACE1005934, PLACE1006076, PLACE1006119, PLACE1006159, PLACE1006164, PLACE1006170, PLACE1006382, PLACE1006492, PLACE1006629, PLACE1006704, PLACE1006731, PLACE1006760, PLACE1006779, PLACE1006795, PLACE1006805, PLACE1006962, PLACE1007045, PLACE1007111, PLACE1007282, PLACE1007386, PLACE1007416, PLACE1007484, PLACE1007544, PLACE1007645, PLACE1007743, PLACE1007746, PLACE1007807, PLACE1007858, PLACE1008002, PLACE1008181, PLACE1008273, PLACE1008368, PLACE1008405, PLACE1008532, PLACE1008568, PLACE1008625, PLACE1008696, PLACE1008867, PLACE1009027, PLACE1009039, PLACE1009045, PLACE1009110, PLACE1009298, PLACE1009328, PLACE1009581, PLACE1009621, PLACE1009622, PLACE1009637, PLACE1009925, PLACE1009935, PLACE1010089, PLACE1010106, PLACE1010152, PLACE1010274, PLACE1010491, PLACE1010629, PLACE1010630, PLACE1010714, PLACE1010739, PLACE1010891, PLACE1010896, PLACE1010925, PLACE1010965, PLACE1011026, PLACE1011046, PLACE1011214, PLACE1011399, PLACE1011433, PLACE1011492, PLACE1011641, PLACE1011649, PLACE1011719, PLACE1011762, PLACE1011858, PLACE1011923, PLACE2000014, PLACE2000039, PLACE2000216, PLACE2000302, PLACE2000317, PLACE2000342, PLACE2000347, PLACE2000379, PLACE3000121, PLACE3000124, PLACE3000160, PLACE3000242, PLACE3000271, PLACE3000353, PLACE3000362, PLACE3000365, PLACE3000400, PLACE3000401, PLACE4000034, PLACE4000089, PLACE4000522, PLACE4000558,
SKNMC1000050, THYRO1000040, THYRO1000197, THYRO1000241, THYRO1000327, THYRO1000394, THYRO1000488, THYRO1000501, THYRO1000585, THYRO1000596, THYRO1000625, THYRO1000805, THYRO1000934, THYRO1001133, THYRO1001134, THYRO1001173, THYRO1001213, THYRO1001262, THYRO1001290, THYRO1001721, Y79AA1000037, Y79AA1000800, Y79AA1000976, Y79AA1001078, Y79AA1001228, Y79AA1001299, Y79AA1001402, Y79AA1001585, Y79AA1001696, Y79AA1001711, Y79AA1001827, Y79AA1001875, Y79AA1002027, Y79AA1002211, Y79AA1002234, Y79AA1002258

[0099] On the other hand, clones of which expression levels decrease by RA/inhibitor are as follows:

HEMBA1000012, HEMBA1000501, HEMBA1000946, HEMBA1003220, HEMBA1003403, HEMBA1003569, HEMBA1003591, HEMBA1003926, HEMBA1004168, HEMBA1004507, HEMBA1005009, HEMBA1005296, HEMBA1005528, HEMBA1005570, HEMBA1006467, HEMBA1006486, HEMBA1006492, HEMBA1007322, HEMBB1000055, HEMBB1000244, HEMBB1001665, MAMMA1000684, MAMMA1001139, MAMMA1001743, NT2RM1000257 NT2RM1000318, NT2RM1000539, NT2RM1000666, NT2RM2000092, NT2RM2000192, NT2RM2000371, NT2RM2000594, NT2RM4000511, NT2RM4001140, NT2RM4001754, NT2RM4001905, NT2RM4001940, NT2RM4002593, NT2RP1000086, NT2RP1000439, NT2RP1001073, NT2RP2000098, NT2RP2000965, NT2RP2001397, NT2RP2002047, NT2RP2004226, NT2RP2004396, NT2RP2004655, NT2RP2005126, NT2RP2005464, NT2RP2005712, NT2RP2005859, NT2RP2005890, NT2RP3000980, NT2RP3001383, NT2RP3001621, NT2RP3002081, NT2RP3002181, NT2RP3002244, NT2RP3002590, NT2RP3003059, NT2RP3004258, NT2RP3004378, NT2RP3004527, NT2RP3004594, NT2RP4001760, NT2RP4001950, NT2RP4002047, NT2RP4002408, NT2RP5003459, OVARC1000004, OVARC1000035, OVARC1000431, OVARC1001051, OVARC1001129, OVARC1001176, OVARC1001261, OVARC1001342, OVARC1001942, OVARC1001943, PLACE1002171, PLACE1002465, PLACE1003190, PLACE1003375, PLACE1004128, PLACE1005026, PLACE1005876, PLACE1005923, PLACE1007257, PLACE1007375, PLACE1007507, PLACE1008941, PLACE1010624, PLACE1011090, PLACE1011219, THYRO1000270, Y79AA1000346, Y79AA1001541

[0100] These clones are also associated with neural differentiation and, therefore, are candidates for genes associated with neurological diseases.

[0101] For example, if the protein encoded by the cDNA of the present invention is a regulatory factor of cellular conditions such as growth and differentiation, it can be used for developing medicines as follows. The protein or antibody provided by the invention is injected into a certain kind of cells by microinjection. Then, using the cells, it is possible to screen low molecular weight compounds by measuring the change in the cellular conditions, or the activation or inhibition of a particular gene. The screening can be performed as follows. First, the protein is expressed and purified as recombinant. The purified protein is microinjected into cells such as various cell lines, or primary culture cells, and the cellular change such as growth and differentiation can be examined. Alternatively, the induction of genes whose expression is known to be associated with a particular change of cellular conditions may be detected by the amount of mRNA or protein. Or, the amount of intracellular molecules (low molecular weight compounds, etc.) that is changed by the function of the gene product (protein) which is known to be associated with a particular change of cellular conditions may be detected. The compounds to be screened (both low and high molecular compounds are acceptable) can be added to the culture media and assessed for their activity by measuring the change of the cellular conditions. Instead of microinjection, cell lines introduced with the gene obtained in the invention can be used for the screening. If the gene product is turn out to be associated with a particular change in the cellular conditions, the change of the product can be used as a measurement for screening. Once a compound is screened out which can activate or inhibit

the function of the protein of the invention, it can be applied for developing medicines.

[0102] If the protein encoded by the cDNA of the present invention is a secretory protein, membrane protein, or protein associated with signal transduction, glycoprotein, transcription, or diseases, it can be used in functional assays for developing medicines.

[0103] In case of a membrane protein, it is most likely to be a protein that functions as a receptor or ligand on the cell surface. Therefore, it is possible to reveal a new relationship between a ligand and receptor by screening the membrane protein of the invention based on the binding activity with the known ligand or receptor. Screening can be performed according to the known methods.

[0104] For example, a ligand against the protein of the invention can be screened in the following manner. Namely, a ligand that binds to a specific protein can be screened by a method comprising the steps of: (a) contacting a test sample with the protein of the invention or a partial peptide thereof, or cells expressing these, and (b) selecting a test sample that binds to said protein, said partial peptide, or said cells.

[0105] On the other hand, for example, screening using cells expressing the protein of the present invention that is a receptor protein can also be performed as follows. It is possible to screen receptors that is capable of binding to a specific protein by using procedures (a) attaching the sample cells to the protein of the invention or its partial peptide, and (b) selecting cells that can bind to the said protein or its partial peptide.

[0106] In a following screening as an example, first the protein of the invention is expressed, and the recombinant protein is purified. Next, the purified protein is labeled, binding assay is performed using a various cell lines or primary cultured cells, and cells that are expressing a receptor are selected (Growth and differentiation factors and their receptors, Shin-Seikagaku Jikken Kouza Vol.7 (1991) Honjyo, Arai, Taniguchi, and Muramatsu edit, p203-236, Tokyo-Kagaku-Doujin). A protein of the invention can be labeled with RI such as ^{125}I, and enzyme (alkaline phosphatase etc.). Alternatively, a protein of the invention may be used without labeling and then detected by using a labeled antibody against the protein. The cells that are selected by the above screening methods, which express a receptor of the protein of the invention, can be used for the further screening of an agonists or antagonists of the said receptor.

[0107] Once the ligand binding to the protein of the invention, the receptor of the protein of the invention or the cells expressing the receptor are obtained by screening, it is possible to screen a compound that binds to the ligand and receptor. Also it is possible to screen a compound that can inhibit both bindings (agonists or antagonists of the receptor, for example) by utilizing the binding activities.

[0108] When the protein of the invention is a receptor, the screening method comprises the steps of (a) contacting the protein of the invention or cells expressing the protein of the invention with the ligand, in the presence of a test sample, (b) detecting the binding activity between said protein or cells expressing said protein and the ligand, and (c) selecting a compound that reduces said binding activity when compared to the activity in the absence of the test sample. Furthermore, when the protein of the invention is a ligand, the screening method comprises the steps of (a) contacting the protein of the invention with its receptor or cells expressing the receptor in the presence of samples, (b) detecting the binding activity between the protein and its receptor or the cells expressing the receptor, and (c) selecting a compound that can potentially reduce the binding activity compared to the activity in the absence of the sample.

[0109] Samples to screen include cell extracts, expressed products from a gene library, synthesized low molecular compound, synthesized peptide, and natural compounds, for example, but are not construed to be listed here. A compound that is isolated by the above screening using a binding activity of the protein of the invention can also be used as a sample.

[0110] A compound isolated by the screening may be a candidate to be an agonist or an antagonist of the receptor of the protein. By utilizing an assay that monitors a change in the intracellular signaling such as phosphorylation which results from reduction of the binding between the protein and its receptor, it is possible to identify whether the obtained compound is an agonist or antagonist of the receptor. Also, the compound may be a candidate of a molecule that can inhibit the interaction between the protein and its associated proteins (including a receptor) in vivo. Such compounds can be used for developing drugs for precaution or cures of a disease with which the protein is associated.

[0111] Secretory proteins may regulate cellular conditions such as growth and differentiation. It is possible to find out a novel factor that regulates cellular conditions by adding the secretory protein of the invention to a certain kind of cell, and performing a screening by utilizing the cellular changes in growth or differentiation, or activation of a particular gene.

[0112] The screening can be performed, for example, as follows. First, the protein of the invention is expressed and purified in a recombinant form. Then, the purified protein is added to a various kind of cell lines or primary cultured cells, and the change in the cell growth and differentiation is monitored. The induction of a particular gene that is known to be involved in a certain cellular change is detected by the amounts of mRNA and protein. Alternatively, the amount of an intracellular molecule (low-molecular-weight compounds, etc.) that is changed by the function of a gene product (protein) that is known to function in a certain cellular change is used for the detection.

[0113] Once the screening reveals that the protein of the invention can regulate cellular conditions or the functions, it is possible to apply the protein as a pharmaceutical and diagnostic medicine for associated diseases by itself or by

altering a part of it into an appropriate composition.

[0114] As is above described for membrane proteins, the secretory protein provided by the invention may be used to explore a novel ligand-receptor interaction using a screening based on the binding activity to a known ligand or receptor. A similar method can be used to identify an agonist or antagonist. The resulting compounds obtained by the methods can be a candidate of a compound that can inhibit the interaction between the protein of the invention and an interacting molecule (including a receptor). The compounds may be able to use as a preventive, therapeutic, and diagnostic medicine for the diseases, in which the protein may play a certain role.

[0115] Proteins associated with signal transduction or transcription may be a factor that affects a certain protein or gene in response to intracellular/extracellular stimuli. It is possible to find out a novel factor that can affect a protein or gene by expressing the protein provided by the invention in a certain types of cells, and performing a screening utilizing the activation of a certain intracellular protein or gene.

[0116] The screening may be performed as follows. First, a transformed cell line expressing the protein is obtained. Then, the transformed cell line and the untransformed original cell line are compared for the changes in the expression of a certain gene by detecting the amount of its mRNA or protein. Alternatively, the amount of an intracellular molecule (low molecular weight compounds) that is changed by the function of a certain gene product (protein) may be used for the detection. Furthermore, the change of the expression of a certain gene can be detected by introducing a fusion gene that comprises a regulatory region of the gene and a marker gene (luciferase, beta-galactosidase, etc.) into a cell, expressing the protein provided by the invention into the cell, and estimating the activity of a marker gene product (protein).

[0117] If the protein or gene of the invention is associated with diseases, it is possible to screen a gene or compound that can regulate its expression and/or activity either directly or indirectly by utilizing the protein of the present invention.

[0118] For example, the protein of the invention is expressed and purified as a recombinant protein. Then, the protein or gene that interacts with the protein of the invention is purified, and screened based on the binding. Alternatively, the screening can be performed by adding with a compound of a candidate of the inhibitor added in advance and monitoring the change of binding activity. In another method, a transcription regulatory region locating in the 5'-upstream of the gene encoding the protein of the invention that is capable of regulating the expression of other genes is obtained, and fused with a marker gene. The fusion is introduced into a cell, and the cell is added with compounds to explore a regulatory factor of the expression of the said gene.

[0119] The compound obtained by the screening can be used for developing pharmaceutical and diagnostic medicines for the diseases with which the protein of the present invention is associated. Similarly, if the regulatory factor obtained in the screening is turn out to be a protein, compounds that can newly affect the expression or activity of the protein may be used as a medicine for the diseases with which the protein of the invention is associated.

[0120] If the protein of the invention has an enzymatic activity, regardless as to whether it is a secretory protein, membrane protein, or proteins associated with signal transduction, glycoprotein, transcription, or diseases, a screening may be performed by adding a compound to the protein of the invention and monitoring the change of the compound. The enzymatic activity may also be utilized to screen a compound that can inhibit the activity of the protein.

[0121] In a screening given as an example, the protein of the invention is expressed and the recombinant protein is purified. Then, compounds are contacted with the purified protein, and the amount of the compound and the reaction products is examined. Alternatively, compounds that are candidates of an inhibitor are pretreated, then a compound (substrate) that can react with the purified protein is added, and the amount of the substrate and the reaction products is examined.

[0122] The compounds obtained in the screening may be used as a medicine for diseases with which the protein of the invention is associated. Also they can be applied for tests that examine whether the protein of the invention functions normally *in vivo*.

[0123] Whether the secretory protein, membrane protein, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein of the present invention is a novel protein associated with diseases or not is determined in another method than described above, by obtaining a specific antibody against the protein of the invention, and examining the relationship between the expression or activity of the protein and a certain disease. In an alternative way, it may be analyzed referred to the methods in "Molecular Diagnosis of Genetic Diseases" (Elles R. edit, (1996) in the series of "Method in Molecular Biology" (Humana Press).

[0124] Proteins associated with diseases are targets of screening as mentioned, and thus are very useful in developing drugs which regulate their expression and activity. Also, the proteins are useful in the medicinal industry as a diagnostic marker of the associated disease or a target of gene therapy.

[0125] Compounds isolated as mentioned above can be administered patients as it is, or after formulated into a pharmaceutical composition according to the known methods. For example, a pharmaceutically acceptable carrier or vehicle, specifically sterilized water, saline, plant oil, emulsifier, or suspending agent can be mixed with the compounds appropriately. The pharmaceutical compositions can be administered to patients by a method known to those skilled in the art, such as intraarterial, intravenous, or subcutaneous injections. The dosage may vary depending on the weight

or age of a patient, or the method of administration, but those skilled in the art can choose an appropriate dosage properly. If the compound is encoded by DNA, the DNA can be cloned into a vector for gene therapy, and used for gene therapy. The dosage of the DNA and the method of its administration may vary depending on the weight or age of a patient, or the symptoms, but those skilled in the art can choose properly.

[0126] The present invention further relates to databases comprising at least a sequence of polynucleotide and/or protein, or a medium recorded in such databases, selected from the sequence data of the nucleotide and/or the amino acids indicated in Table 350 and Table 351.

The term "database" means a set of accumulated information as machine-searchable and readable information of nucleotide sequence. The databases of the present invention comprise at least one of the novel nucleotide sequences of polynucleotides provided by the present invention. The databases of the present invention can consist of only the sequence data of the novel polynucleotides provided by the present invention or can comprise other information on nucleotide sequences of known full-length cDNAs or ESTs. The databases of the present invention can be comprised of not only the information on the nucleotide sequences but also the information on the gene functions revealed by the present invention. Additional information such as names of DNA clones carrying the full-length cDNAs can be recorded or linked together with the sequence data in the databases.

[0127] The database of the present invention is useful for gaining complete gene sequence information from partial sequence information of a gene of interest. The database of the present invention comprises nucleotide sequence information of full-length cDNAs. Consequently, by comparing the information in this database with the nucleotide sequence of a partial gene fragment yielded by differential display method or subtraction method, the information on the full-length nucleotide sequence of interest can be gained from the sequence of the partial fragment as a starting clue.

[0128] The sequence information of the full-length cDNAs constituting the database of the present invention contains not only the information on the complete sequences but also extra information on expression frequency of the genes as well as homology of the genes to known genes and known proteins. Thus the extra information facilitates rapid functional analyses of partial gene fragments. Further, the information on human genes is accumulated in the database of the present invention, and therefore, the database is useful for isolating a human homologue of a gene originating from other species. The human homologue can be isolated based on the nucleotide sequence of the gene from the original species.

[0129] At present, information on a wide variety of gene fragments can be obtained by differential display method and subtraction method. In general, these gene fragments are utilized as tools for isolating the full-length sequences thereof. When the gene fragment corresponds to an already-known gene, the full-length sequence is easily obtained by comparing the partial sequence with the information in known databases. However, when there exists no information corresponding to the partial sequence of interest in the known databases, cDNA cloning should be carried out for the full-length cDNA. It is often difficult to obtain the full-length nucleotide sequence using the partial sequence information as an initial clue. If the full-length of the gene is not available, the amino acid sequence of the protein encoded by the gene remains unidentified. Thus the database of the present invention can contribute to the identification of full-length cDNAs corresponding to gene fragments, which cannot be revealed by using databases of known genes.

[0130] The present invention has provided 5602 novel full-length cDNA clones, and primers for synthesizing the cDNA. As has not yet proceeded the isolation of full-length cDNA within the human, the invention has great significance. The full-length cDNA clones contain the translation initiation site, and thus provide a useful information for analysis of protein functions.

[0131] The cDNA clones are assumed to encode proteins such as secretory proteins, membrane proteins, signal transduction-associated protein, glycoprotein-associated protein, or transcription-associated protein, etc., which have important functions in vivo, and also predicted to be associated with many diseases. The genes and proteins associated with diseases are useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as a target of gene therapy.

[0132] The invention is illustrated more specifically with reference to the following examples, but is not to be construed as being limited thereto.

EXAMPLE 1

Construction of a cDNA library by the oligo-capping method.

[0133] The NT-2 neuron progenitor cells (Stratagene), a teratocarcinoma cell line from human embryo testis, which can differentiate into neurons by the treatment with retinoic acid were used.

The NT-2 cells were cultured according to the manufacturer's instructions as follows.

(1) NT-2 cells were cultured without induction by retinoic acid treatment (NT2RM1, NT2RM2, NT2RM4).

(2) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 48 hours (NT2RP1).

(3) After cultured, NT-2 cells were induced by adding retinoic acid, and then were cultured for 2 weeks (NT2RP2, NT2RP3, NT2RP4, NT2RP5).

[0134] Also, the human neuroblastoma cell line SK-N-MC (ATCC HTB-10) (SKNMC1), and human retinoblastoma cell line Y79 (ATCC HTB-18) (Y79AA1) were cultured according to the culture conditions described in the ATCC catalogue (http://www.atcc.org/). The cells were harvested separately, and mRNA was extracted from each cell by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0135] Similarly, human placenta (PLACE1, PLACE2, PLACE3, PLACE4), human ovary cancer tissue (OVARC1), tissues from human embryo at 10 weeks, which is enriched with head (HEMBA1), or body (HEMBB1), human mammary gland (MAMMA1), human thyroid gland (THYRO1), and primary cultured cells of human blood vessel endothelium (VESEN1) were used to extract mRNA by the method described in the literature (Molecular Cloning 2nd edition. (1989) Sambrook J., Fritsch, E.F., and Maniatis T., Cold Spring Harbor Laboratory Press). Furthermore, poly(A)$^+$RNA was purified from the mRNA using oligo-dT cellulose.

[0136] Each poly(A)$^+$RNA was used to construct a cDNA library by the oligo-capping method (Maruyama M. and Sugano S. (1994) Gene, 138: 171-174). Using the Oligo-cap linker (SEQ ID NO: 10464) and the Oligo-dT primer (SEQ ID NO: 10465), bacterial alkaline phosphatase (BAP) treatment, tobacco acid phosphatase (TAP) treatment, RNA ligation, the first strand cDNA synthesis, and removal of RNA were performed as described in the reference (Suzuki and Kanno (1996) Protein Nucleic acid and Enzyme, 41: 197-201; Suzuki Y. et al. (1997) Gene, 200: 149-156). Next, 5'- and 3'-PCR primers (SEQ ID NO: 10466, and 10467, respectively) were used for performing PCR to convert the cDNA into double stranded cDNA, which was then digested with SfiI. Then, the DraIII-cleaved pUC19FL3 vector (Figure 1; for NT2RM1, and NT2RP1), or the DraIII-cleaved pME18SFL3 (Figure 1) (GenBank AB009864, expression vector; for NT2RM2, NT2RM4, NT2RP2, NT2RP3, NT2RP4, NT2RP5, SKNMC1, Y79AA1, PLACE1, PLACE2, PLACE3, PLACE4, OVARC1, HEMBA1, HEMBB1, MAMMA1, THYRO1, and VESEN1) was used for cloning the cDNA in a unidirectional manner, and cDNA libraries were obtained. The nucleotide sequence of the 5'- and 3'- ends of the cDNA clones was analyzed with a DNA sequencer (ABI PRISM 377, PE Biosystems) after sequencing reactions were performed with the DNA sequencing reagents (Dye Terminator Cycle Sequencing FS Ready Reaction Kit, dRhodamine Terminator Cycle Sequencing FS Ready Reaction Kit, or BigDye Terminator Cycle Sequencing FS Ready Reaction Kit, PE Biosystems), according to the instructions. The data were compiled into a database.

[0137] The full-length-enriched cDNA libraries except those for NT2RM1 and NT2RP1 were constructed using eukaryotic expression vector pME18SFL3. The vector contains SRα promoter and SV40 small t intron in the upstream of the cloning site, and SV40 polyA added signal sequence site in the downstream. As the cloning site of pME18SFL3 has asymmetrical DraIII sites, and the ends of cDNA fragments contain SfiI sites complementary to the DraIII sites, the cloned cDNA fragments can be inserted into the downstream of the SRα promoter unidirectionally. Therefore, clones containing full-length cDNA can be expressed transiently by introducing the obtained plasmid directly into COS cells. Thus, the clones can be analyzed very easily in terms of the proteins that are the gene products of the clones, or in terms of the biological activities of the proteins.

[0138] Herein, the cDNA libraries and the name of each clone are related as shown in Table 3. Therein, "xxxxxx" represents the clone number of six digits. Thus, the sequences are named by the library name, the clone number plus F- for the 5'-end, or R- for the 3'-end.

NT2RP2:		
NT2RP2xxxxxx	F-NT2RP2xxxxxx	R-NT2RP2xxxxxx
NT2RP3:		
NT2RP3xxxxxx	F-NT2RP3xxxxxx	R-NT2RP3xxxxxx
NT2RP4:		
NT2RP4xxxxxx	F-NT2RP4xxxxxx	R-NT2RP4xxxxxx
NT2RP5:		
NT2RP5xxxxxx	F-NT2RP5xxxxxx	R-NT2RP5xxxxxx
SKNMC1:		
SKNMC1xxxxxx	F-SKNMC1xxxxxx	R-SKNMC1xxxxxx
Y79AA1:		
Y79AA1xxxxxx	F-Y79AA1xxxxxx	R-Y79AA1xxxxxx
PLACE1:		
PLACE1xxxxxx	F-PLACE1xxxxxx	R-PLACE1xxxxxx
PLACE2:		
PLACE2xxxxxx	F-PLACE2xxxxxx	R-PLACE2xxxxxx
PLACE3:		
PLACE3xxxxxx	F-PLACE3xxxxxx	R-PLACE3xxxxxx
PLACE4:		
PLACE4xxxxxx	F-PLACE4xxxxxx	R-PLACE4xxxxxx
OVARC1:		
OVARC1xxxxxx	F-OVARC1xxxxxx	R-OVARC1xxxxxx
HEMBA1:		
HEMBA1xxxxxx	F-HEMBA1xxxxxx	R-HEMBA1xxxxxx
HEMBB1:		
HEMBB1xxxxxx	F-HEMBB1xxxxxx	R-HEMBB1xxxxxx
MAMMA1:		
MAMMA1xxxxxx	F-MAMMA1xxxxxx	R-MAMMA1xxxxxx
THYRO1:		
THYRO1xxxxxx	F-THYRO1xxxxxx	R-THYRO1xxxxxx
VESEN1:		
VESEN1xxxxxx	F-VESEN1xxxxxx	R-VESEN1xxxxxx

EXAMPLE 2

Estimation of the fullness ratio at the 5'-ends of the clones contained in the cDNA libraries constructed by the oligo-capping method.

[0139] The fullness ratio at the 5'-end sequence of the 59,823 clones in the human cDNA libraries constructed by the oligo-capping method was determined as follows. Of all the clones whose 5'-end sequences were found in those of known human mRNA in the public database, a clone was judged to be "full-length", if it had a longer 5'-end sequence than that of the known human mRNA, or, even though the 5'-end sequence was shorter, if it contained the translation initiation codon. A clone which did not contain the translation initiation codon was judged to be "not-full-length". The fullness ratio ((the number of full-length clones)/(the number of full-length and not-full-length clones)) at the 5'-end of the cDNA clones from each library was determined by comparing with the known human mRNA. As a result, the fullness

ratio of the 5'-ends was 63.5%. The result indicates that the fullness ratio at the 5'-end sequence was extremely high.

EXAMPLE 3

Assessment of the fullness ratio of the 5'-end of the cDNA by the ATGpr and the ESTiMateFL.

[0140] The ATGpr, developed by Salamov A.A., Nishikawa T., and Swindells M.B. in the Helix Research Institute, is a program for prediction of the translation initiation codon based on the characteristics of the sequences in the vicinity of the ATG codon. The results are shown with expectations (also described as ATGpr1 below) that an ATG is a true initiation codon (0.05-0.94) (can be described as ATGpr1). When the program was applied to the 5'-end sequences of the clones from the cDNA library that was obtained by the oligo-capping method and that had 65% fullness ratio, the sensitivity and specificity of estimation of a full-length clone (clone containing the N-terminal end of ORF) were improved to 82-83% by selecting only clones having the ATGpr1 score 0.6 or higher.

[0141] Furthermore, the program was used to assess the fullness of 18,959 clones in the human libraries obtained here, which have 5'-ends matched to a known human mRNA.

[0142] Briefly, the maximal ATGpr1 score of the clones was determined, and then their 5'-end sequence was compared with the known human mRNA to estimate whether the clone is full-length or not. The result is shown in Table 4.

[0143] Based on the knowledge that known mRNAs, in general, are highly expressed in the cell, similar estimation was performed with genes having a low number in the EST hit, which represent relatively low abundant mRNAs, and the result is shown in Table 5.

[0144] In the table, the number of full-length clones indicate that of clones containing the N-terminal end of ORF, and so does the number of not-full-length clones that of clones without the N-terminal end of ORF. The fullness ratio represents (the number of full-length clones)/(the number of full-length clones plus the number of not-full-length clones).

Table 4

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having a matched 5'-end with that of a known mRNA.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	11,193	9,346	83.5%
>=0.50	13,369	10,549	78.9%
>=0.30	15,489	11,340	73.2%
>=0.15	17,394	11,811	67.9%
>=0.00	18,959	12,046	63.5%

Table 5

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequences of the clones obtained from human cDNA libraries constructed by the oligo-capping method; clones having 5 EST hits or less among the clones having a matched 5'-end with that of a known mRNA.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	2,801	1,934	69.0%
>=0.50	3,683	2,393	65.0%
>=0.30	4,683	2,707	57.8%
>=0.15	5,559	2,890	52.0%
>=0.00	6,113	3,013	49.8%

[0145] Next, the ESTiMateFL was used for the estimation. The ESTiMateFL, developed by Nishikawa and Ota in the Helix Research Institute, is a method for the selection of a clone with high fullness ratio by comparing with the 5'-end or 3'-end sequences of ESTs in the public database.

[0146] By the method, a cDNA clone is judged to be most likely not to be full-length if there exist any ESTs which

have longer 5'-end or 3'-end sequences than the clone. The method is systematized for high throughput analysis. A clone is judged to be full-length if the clone has a longer 5'-end sequence than ESTs in the public database. Even if a clone has a shorter 5'-end, the clone is judged to be full-length if the difference in length is within 50 bases, and otherwise judged not to be full-length, for convenience.

[0147] In case of the clones whose 5'-end sequence is matching with the known mRNA, 80% of the clones judged to be full-length by comparing with ESTs was also judged to be full-length by comparing with the known mRNA. Also, 80% of the clones judged to be not full-length by comparing with ESTs was also judged to be not full-length by comparing with the known mRNA.

[0148] The precision of the estimation by comparing with ESTs is improved with increasing number of ESTs to be compared. However, in case that a limited number of ESTs are available, the reliability becomes low. Thus, the method is effective in excluding clones with high probability of being not-full-length, from the cDNA clones that is synthesized by the oligo-capping method and that have the 5'-end sequences with about 60 % fullness ratio. In particular, the ESTiMateFL is efficiently used to estimate the fullness ratio at the 3'-end sequence of cDNA of a human unknown mRNA which has a significant number of EST deposits in the public database.

[0149] The 18,959 clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, were estimated by using the ATGpr and ESTiMateFL. Briefly, the 5'-end sequence of the respective clone was analyzed to obtain the maximal ATGpr1 score, and compared with the ORF of the known human mRNA that matches with it to determine whether the clone is full-length or not. Then, the 5'-end sequence of the respective clone was analyzed by the ESTiMateFL to judge whether the clone is full-length or not. Specifically, the 5'-end sequences of the 18,959 clones were compared with those of ESTs by the ESTiMateFL and the clones other than those that are not full-length were selected. Then, the selected clones were used to analyze the relationship between the ATGpr and the fullness ratio. The result was summarized in Table 6. Also, among the selected, the clones in which the number of the EST hit is not more than 5 were selected and analyzed. The result was summarized in Table 7, which represents the result of the analysis of mRNA with relatively low abundance.

[0150] Therein, the number of being full-length, the number of being not full-length, and the fullness ratio indicate the number of the clones that contain the N-terminus of the ORF, the number of the clones that do not contain the N-terminus of the ORF, and (the number of being full-length)/(the number of being full-length) plus (the number of being not full-length), respectively.

Table 6

The maximal ATGpr1 score and the fullness ratio of the 5'-end sequence in the clones isolated from human cDNA libraries constructed by the oligo-capping method, which have the 5'-end sequence matched with a known human mRNA, and also other than those being not full-length according to the comparison with ESTs.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	9,068	8,349	92.1%
>=0.50	10,345	9,318	90.1%
>=0.30	11,425	9,964	87.2%
>=0.15	12,254	10,335	84.3%
>=0.00	12,785	10,484	82.0%

Table 7

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.

maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.70	1,959	1,510	77.1%
>=0.50	2,469	1,821	73.8%
>=0.30	2,975	2,046	68.8%
>=0.15	3,368	2,164	64.3%

Table 7 (continued)

Maximal ATGpr1 score and fullness ratio of the 5'-end sequence of the clones, which were isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA, in which the number of the EST hit is not more than 5.			
maximal ATGpr1 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.00	3,661	2,226	60.8%

[0151] The 19,226 clones, isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to that of a known human mRNA were estimated by the ATGpr2, and the correlation between the score and the fullness ratio was estimated. Specifically, the maximal ATGpr2 score of the clones identical to a known human mRNA was determined, and then their fullness ratio was estimated by comparing the 5'-ends with ORF of known human mRNA. The result was shown in Table 8.

Table 8

Maximal ATGpr2 score and fullness ratio of the 5'-end sequence of the clones, which are isolated from the human cDNA libraries constructed by the oligo-capping method, whose 5'-end sequence is identical to a known human mRNA.			
maximal ATGpr2 score	number of (full-length clones plus not-full-length clones)	number of full-length clones	fullness ratio
>=0.30	10,748	8,031	74.7%
>=0.15	16,383	11,226	68.5%
>=0.00	19,226	12,285	63.9%

[0152] According to the above results, it was found that, in case of using clones isolated from human cDNA libraries constructed by the oligo-capping method, the fullness ratio of the clones that have low score in the ATGpr can be improved by estimating their 5'-end sequence using the combination of the ATGpr and the ESTiMateFL. Therefore, the method was applied to select a cDNA clone with high fullness ratio.

EXAMPLE 4

Clustering of the 5'-end and 3'-end sequences of cDNA clones.

[0153] The 5'-end and 3'-end sequences of cDNA clones were obtained, and clustered separately. The single pass data of the nucleotide sequence of the 5'-end and 3'-end was subject to the BLAST search between the sequence data of all the clones synthesized in example 1, and the clones considered to be originating from the same gene were put together into a group. If the 5'-end of a clone contains the consensus sequence of 300 bases or more with identity 95% or more, or the 3'-end contains the consensus sequence of 200 bases or more and having identity 90% or more, the clones were put in the same group.

[0154] The groups of the 5'-end sequence and the 3'-end sequence were further clustered so as that the groups from the same clone can be in the same group (cluster).

EXAMPLE 5

Characterization of the cloned sequence.

[0155] The data of the 5'-end sequence of the cloned sequence was characterized by the following way:

(1) examining whether it is identical to those of mRNA from human and other species (including authorized sequences) and human EST by the BLAST homology search of the GenBank,
(2) examining whether it has longer 5'-end than those of human mRNA and human EST,
(3) determining the scores in the ATGpr1 and ATGpr2 programs of all the initiation codons in the 5'-end sequence, and

(4) determining the number of the human EST clone(s) that is judged to be identical by the BLAST homology search of the GenBank.

[0156] The data of the 3'-end sequence of the cloned sequence was characterized by the above (1) and (4).

[0157] These characterized data were used for the final selection of the clones.

EXAMPLE 6

Identity to the human mRNA and human EST, and comparison of the length of the 5'-end.

[0158] The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of mRNA from human or other species when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 94% or more. The 5'-end and 3'-end sequences of the cloned sequence was judged to be identical to those of human EST when the sequence to compare has the length of 200 bases or longer, and the obtained homology is 90% or more.

[0159] The sequence of the clone was judged to be full-length in comparison with human mRNA when the sequence has longer 5'-end, or it contains the translation initiation site. The sequence of the clone was judged to be full-length in comparison with human EST in the database when the sequence has longer 5'-end, or while it has shorter end, the difference in length between the two sequences is 50 bases or less. The other clones were judged to be not full-length.

EXAMPLE 7

Prediction of the fullness ratio by the ATGpr.

[0160] The score in the ATGpr1 is the expectation to be full-length based on calculations, and the higher score reflects the higher probability to be full-length as shown in Example 3. The maximal ATGpr1 score and the maximal ATGpr2 score represent the score obtained with all the initiation codons contained in the 5'-end sequence of the cloned sequence, and were used for the characterization.

EXAMPLE 8

Prediction of the novelty using the number of the identical ESTs by the homology search.

[0161] For both the 5'-end and 3'-end sequences of the clones, the number of the identical ESTs was determined by the homology search on the GenBank. Human ESTs were judged to be identical when the EST has a sequence of 200 nucleotides or more with 90% or more matching with the 5'-end sequence. The number of the identical ESTs were used for characterization and as an index of novelty. The clone having not identical sequence at the 5'-end and 3'-end sequences to those of mRNA as well as those of ESTs is a gene encoding a novel protein. Similarly, a clone having either the 5'-end or the 3'-end sequences, which has low number of the identical ESTs, is judged to be a gene encoding a novel protein.

EXAMPLE 9

Characterization of clusters.

[0162] The clusters of the groups of the 5'-end and 3'-end sequences were characterized according to the following criteria.

(1) Whether it is identical to the mRNA sequences from human or other species (including authorized sequences), or human ESTs by the BLAST search of the GenBank.
A cluster containing at least one sequence of all the 5'-end and 3'-end sequences, which is identical to one of the mRNA sequences, was regarded to be the same cluster of the mRNA sequence.
(2) Whether it has longer 5'-end than human mRNA sequence and human ESTs.
When all the 5'-end sequences contained in a cluster are judged to be not full-length compared with the mRNA sequences and human ESTs, the cluster was regarded as being not full-length.
(3) The scores in the ATGpr1 and ATGpr2 using all the initiation codons contained in the 5'-end sequences.
The maximal ATGpr1 score among those of all the 5'-end sequences in a cluster was determined as the ATGpr1 score of the cluster. The ATGpr2 score of the cluster was also determined in the same way.

(4) The number of the identical human ESTs determined by the BLAST search of the GenBank.

[0163] The maximum number was determined in the numbers of ESTs identical to each of 5'-end sequences contained in a cluster. The number of the ESTs identical to the 5'-end sequences in the cluster was defined as the maximum number. The number of the ESTs identical to the 3'-end sequences in a cluster was determined in the same way.

EXAMPLE 10

Methods for selection of the clusters by the characteristics.

[0164] Data obtained by the characterization described above was used to discard the clusters that are identical to any mRNA sequence from human and other species (including authorized sequences), or those clusters that are not full-length. From the rest of the clusters, the clusters that fulfill any of the following conditions were selected.

(a) A cluster in which the number of the identical ESTs for the 5'-end sequence is 20 or less, and the ATGpr1 score exceeds 0.3.
(b) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for both the 5'-end sequence and the 3'-end sequence is 5 or less, and multiple clones are contained.
(c) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is 0, and the number of the identical ESTs for the 3'-end sequence is not less than 1.
(d) A cluster having the ATGpr1 score not more than 0.3, in which the number of the identical ESTs for the 5'-end sequence is not less than 1 and not more than 5, and the number of the identical ESTs for the 3'-end sequence is 0.

[0165] The clusters selected by (a) contain at least one clone that is novel and having high fullness ratio. The clusters selected by (b), (c), and (d) contain at least one clone that is novel and having low fullness ratio, but is still full-length.

EXAMPLE 11

Methods for selection of clones from clusters.

[0166] In the clusters comprising a single clone, the clone was selected.

[0167] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score higher than 0.3, a clone with the highest score was selected.

[0168] In the clusters comprising multiple clones, in which multiple clones have the ATGpr1 score not more than 0.3, a clone with the highest ATGpr2 score was selected, if the score was higher than 0.3.

[0169] In the clusters comprising multiple clones, in which the clones have the scores not more than 0.3 in both the ATGpr1 and the ATGpr2, a clone with the highest scores in both the ATGpr1 and ATGpr2 was selected.

[0170] In the clusters comprising multiple clones, in which the above selection by the ATGpr score was not applicable, selected was a clone having longer 5'-end by assembling the 5'-end sequence, 3'-end sequence, and human ESTs. For assembling, the Sequencher™ (Hitachi Soft Engineering) was used. When even the selection by assembling failed, all the clones were judged to be full-length.

[0171] As a result, 3690 clones were the clones that have the maximal ATGpr1 score higher than 0.3. On the other hand, 477 clones were the clones that have the maximal ATGpr1 score not more than 0.3, and the maximal ATGpr2 score higher than 0.3. The number of the clones having the highest scores in both the ATGpr1 and ATGpr2, while the scores were not more than 0.3, were 97. The number of the clones which were not selected by the ATGpr scores, but were selected by assembling the 5'-end sequence, 3'-end sequence, and human ESTs, were 117. The clones that have the score in both the ATGpr1 and ATGpr2 not more than 0.3, but were selected because the cluster comprises a single clone, were 1166. In the clones, at least either of the 5'-end or 3'-end sequence was not identical to any of human ESTs. Some clones were selected because the cluster comprises a single clone, or by assembling, in which there is no ATG codon (9 clones: HEMBA1001960, HEMBA106569, HEMBB1001454, NT2PR2002839, NT2RP2005325, NT2RP2006323, PLACE1004506, PLACE1005526, and THYRO1001177). The sequences that do not contain the ATG codon were considered to be corresponding to the 5'-UTR. Although the clones do not have the scores in the ATGpr1 and ATGpr2, the clones were yet judged to be full-length according to the fullness ratio, as shown in Table 4, 5, 6, 7, and 8. The above clones that were finally judged to be full-length were classified into 11 groups according to the following criteria.

Group (1): 1516 clones
Among the 3690 clones having the maximal ATGpr1 score higher than 0.3, the following 1516 clones were having

NT2RM1001008, NT2RM2001896, NT2RM4000024, NT2RM4000061, NT2RM4000155, NT2RM4000169, NT2RM4000229, NT2RM4000290, NT2RM4000354, NT2RM4000895, NT2RM4001032, NT2RM400104 7, NT2RM4001116, NT2RM4001140, NT2RM4001200, NT2RM4001384, NT2RM4001412, NT2RM40014 83, NT2RM4001715, NT2RM4001783, NT2RM4001979, NT2RM4002034, NT2RM4002044, NT2RM4002 145, NT2RM4002344, NT2RM4002452,
NT2RP2000006, NT2RP2000008, NT2RP2000054, NT2RP2000079, NT2RP2000097, NT2RP2000126 NT2RP2000224, NT2RP2000274, NT2RP2000764, NT2RP2000812, NT2RP2000819, NT2RP200084 5, NT2RP2000863, NT2RP2000880, NT2RP2001127, NT2RP2001218, NT2RP2001233, NT2RP20013 94, NT2RP2001420, NT2RP2001576, NT2RP2001597, NT2RP2001721, NT2RP2001907, NT2RP2002 046, NT2RP2002312, NT2RP2002325, NT2RP2002503, NT2RP2002537, NT2RP2002862, NT2RP200 2925, NT2RP2002939, NT2RP2002954, NT2RP2002986, NT2RP2003034, NT2RP2003125, NT2RP20 03286, NT2RP2003293, NT2RP2003347, NT2RP2003433, NT2RP2003445, NT2RP2003543, NT2RP2 003781, NT2RP2004066, NT2RP2004316, NT2RP2004392, NT2RP2004897, NT2RP2004999, NT2RP 2005003, NT2RP2005393, NT2RP2005520, NT2RP2005722, NT2RP2005752, NT2RP2005763, NT2R P2006023, NT2RP2006186, NT2RP2006565,
NT2RP3000527, NT2RP3000562, NT2RP3000590, NT2RP3000596, NT2RP3000599, NT2RP3001004, NT2RP3001126, NT2RP3001150, NT2RP3001392, NT2RP3001407, NT2RP3001457, NT2RP300175 3, NT2RP3001929, NT2RP3001969, NT2RP3002151, NT2RP3002303, NT2RP3002484, NT2RP30025 90, NT2RP3002660, NT2RP3003078, NT2RP3003204, NT2RP3003251, NT2RP3003411, NT2RP3003 831, NT2RP3003870, NT2RP3003876, NT2RP3004093, NT2RP3004246, NT2RP3004253, NT2RP300 4348, NT2RP3004504, NT2RP3004507, NT2RP4000312, NT2RP4000518, NT2RP4000781, NT2RP40 00975, NT2RP4000997, NT2RP4002408, NT2RP5003512,
OVARC1000060, OVARC1000411, OVARC1000440, OVARC1000461, OVARC1000703, OVARC1000846, OVARC1000876, OVARC1000915, OVARC1001040, OVARC1001113, OVARC1001167, OVARC100117 0, OVARC1001188, OVARC1001271, OVARC1001329, OVARC1001610, OVARC1001767, OVARC10018 20, OVARC1001879, OVARC1002138,
PLACE1000014, PLACE1000048, PLACE1000420, PLACE1000588, PLACE1000596, PLACE1000636, PLACE1000755, PLACE1000786, PLACE1000849, PLACE1000909, PLACE1001000, PLACE100124 1, PLACE1001387, PLACE1001503, PLACE1001551, PLACE1001570, PLACE1001602, PLACE10016 10, PLACE1001632, PLACE1001989, PLACE1002115, PLACE1002465, PLACE1002532, PLACE1002 851, PLACE1002991, PLACE1002993, PLACE1003025, PLACE1003342, PLACE1003553, PLACE100 3605, PLACE1003669, PLACE1003723, PLACE1003738, PLACE1003762, PLACE1003783, PLACE10 04104, PLACE1004114, PLACE1004149, PLACE1004197, PLACE1004473, PLACE1004510, PLACE1 004645, PLACE1004672, PLACE1004868,
PLACE1005313, PLACE1005374, PLACE1005834, PLACE1005921, PLACE1005936, PLACE1005966, PLACE1006157, PLACE1006225, PLACE1006239, PLACE1006248, PLACE1006445, PLACE100653 1, PLACE1006626, PLACE1006731, PLACE1006901, PLACE1006961, PLACE1006966, PLACE10073 17, PLACE1007375, PLACE1007460, PLACE1007544, PLACE1007583, PLACE1007791, PLACE1007 843, PLACE1007897, PLACE1008129, PLACE1008309, PLACE1008401, PLACE1008402, PLACE100 8532, PLACE1008627, PLACE1008808, PLACE1008902, PLACE1008934, PLACE1009099, PLACE10 09130, PLACE1009166, PLACE1009659, PLACE1009665, PLACE1009708, PLACE1009794, PLACE1 009886, PLACE1009908, PLACE1010202, PLACE1010580, PLACE1010661, PLACE1010811, PLACE 1010917, PLACE1010942, PLACE1010965, PLACE1011026, PLACE1011325, PLACE1011472, PLAC E1011563, PLACE1011664, PLACE1011682, PLACE1011982, PLACE4000049, PLACE4000300, PLA CE4000558,
THYRO1000368, THYRO1000662, THYRO1000712, THYRO1000783, THYRO1000952, THYRO1000988 THYRO1001661, THYRO1001854, Y79AA1000037, Y79AA1000059, Y79AA1000985, Y79AA100110, 5, Y79AA1001177, Y79AA1001211, Y79AA1001281, Y79AA1001533, Y79AA1001923, Y79AA10020 83, Y79AA1002204, Y79AA1002407,

Group (3): 1797 clones

Among the 3690 clones, the following 1797 clones were full-length, and novel clones, in which the number of the identical human ESTs for the 5'-end sequence is not more than 20 (except clones in which at least either of the 5'-end or 3'-end sequence, or both of them are not identical to any of human ESTs, and clones in which the number of the identical human ESTs for both the 5'-end and 3'-end sequences is 1 or higher and not more than 5).

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000076, HEMBA1000141, HEMBA1000168, HEMBA1000185, HEMBA1000307, HEMBA1000327, HEMBA1000356, HEMBA100038 7, HEMBA1000456, HEMBA1000460, HEMBA1000490, HEMBA1000491, HEMBA1000501, HEMBA10005 20, HEMBA1000561, HEMBA1000588, HEMBA1000591, HEMBA1000592, HEMBA1000608, HEMBA1000 636,

PLACE1000769, PLACE1000785, PLACE1000793, PLACE1000798, PLACE100 0856, PLACE1000863, PLACE1000977, PLACE1000987, PLACE1001054, PLACE1001092, PLACE10 01168, PLACE1001185, PLACE1001238, PLACE1001294, PLACE1001304, PLACE1001351, PLACE1 001383, PLACE1001399, PLACE1001412, PLACE1001608, PLACE1001692, PLACE1001761, PLACE 1001781, PLACE1001817, PLACE1001844, PLACE1001869, PLACE1001920,

PLACE1002046, PLACE1002072, PLACE1002090, PLACE1002140, PLACE1002171, PLACE1002342, PLACE1002395, PLACE1002499, PLACE1002571, PLACE1002722, PLACE1002794, PLACE100281 1, PLACE1002815, PLACE1002816, PLACE1002834, PLACE1002908, PLACE1002996, PLACE10030 27, PLACE1003092, PLACE1003100, PLACE1003136, PLACE1003176, PLACE1003200, PLACE1003 296, PLACE1003302, PLACE1003353, PLACE1003394, PLACE1003454, PLACE1003537, PLACE100 3592, PLACE1003596, PLACE1003602, PLACE1003625, PLACE1003704, PLACE1003886, PLACE10 03892, PLACE1003903, PLACE1003915, PLACE1003923, PLACE1003968,

PLACE1004103, PLACE1004183, PLACE1004258, PLACE1004316, PLACE1004358, PLACE1004376, PLACE1004405, PLACE1004437, PLACE1004550, PLACE1004629, PLACE1004674, PLACE100473 6, PLACE1004777, PLACE1004814, PLACE1004902, PLACE1004930, PLACE1004969, PLACE10049 82, PLACE1005027, PLACE1005055, PLACE1005066, PLACE1005101, PLACE1005102, PLACE1005 181, PLACE1005187, PLACE1005261, PLACE1005287, PLACE1005305, PLACE1005308, PLACE100 5327, PLACE1005335, PLACE1005373, PLACE1005550, PLACE1005557, PLACE1005595, PLACE10 05603, PLACE1005623, PLACE1005630, PLACE1005698, PLACE1005727, PLACE1005739, PLACE1 005803, PLACE1005813, PLACE1005851, PLACE1005955,

PLACE1006040, PLACE1006119, PLACE1006139, PLACE1006159, PLACE1006167, PLACE1006196, PLACE1006236, PLACE1006246, PLACE1006325, PLACE1006335, PLACE1006469, PLACE100648 8, PLACE1006492, PLACE1006615, PLACE1006678, PLACE1006819, PLACE1006883, PLACE10069 17, PLACE1006989, PLACE1007021, PLACE1007053, PLACE1007105, PLACE1007178, PLACE1007 238, PLACE1007239, PLACE1007243, PLACE1007282, PLACE1007367, PLACE1007386, PLACE100 7402, PLACE1007409, PLACE1007416, PLACE1007454, PLACE1007507, PLACE1007511, PLACE10 07547, PLACE1007598, PLACE1007621, PLACE1007632, PLACE1007645, PLACE1007649, PLACE1 007688, PLACE1007690, PLACE1007697, PLACE1007705, PLACE1007706, PLACE1007725, PLACE 1007730, PLACE1007746, PLACE1007846, PLACE1007858, PLACE1007908, PLACE1007954, PLAC E1007955, PLACE1007958, PLACE1007969, PLACE1007990,

PLACE1008044, PLACE1008122, PLACE1008132, PLACE1008198, PLACE1008209, PLACE1008356, PLACE1008368, PLACE1008398, PLACE1008429, PLACE1008524, PLACE1008531, PLACE100856 8, PLACE1008603, PLACE1008629, PLACE1008650, PLACE1009027, PLACE1009045, PLACE10090 60, PLACE1009091, PLACE1009186, PLACE1009298, PLACE1009319, PLACE1009338, PLACE1009 444, PLACE1009468, PLACE1009476, PLACE1009571, PLACE1009581, PLACE1009596, PLACE100 9622, PLACE1009670, PLACE1009721, PLACE1009731, PLACE1009763, PLACE1009845, PLACE10 09921, PLACE1009995,

PLACE1010023, PLACE1010031, PLACE1010053, PLACE1010074, PLACE1010076, PLACE1010096, PLACE1010102, PLACE1010105, PLACE1010106, PLACE1010134, PLACE1010152, PLACE101019 4, PLACE1010274, PLACE1010362, PLACE1010364, PLACE1010383, PLACE1010491, PLACE10104 92, PLACE1010522, PLACE1010529, PLACE1010599, PLACE1010622, PLACE1010630, PLACE1010 720, PLACE1010761, PLACE1010771, PLACE1010786, PLACE1010800, PLACE1010833, PLACE101 0856, PLACE1010857, PLACE1010870, PLACE1010877, PLACE1010925, PLACE1010944, PLACE10 10960, PLACE1011041, PLACE1011090, PLACE1011160, PLACE1011214, PLACE1011219, PLACE1 011221, PLACE1011263, PLACE1011291, PLACE1011310, PLACE1011332, PLACE1011371, PLACE 1011433, PLACE1011477, PLACE1011586, PLACE1011646, PLACE1011675, PLACE1011858, PLAC E1011923,

PLACE2000007, PLACE2000021, PLACE2000030, PLACE2000164, PLACE2000172, PLACE2000302, PLACE2000341, PLACE2000399, PLACE2000404, PLACE2000427, PLACE3000009, PLACE300012 1, PLACE3000148, PLACE3000156, PLACE3000160, PLACE3000197, PLACE3000226, PLACE30002 42, PLACE3000339, PLACE3000353, PLACE3000413, PLACE3000477, PLACE4000009, PLACE4000 034, PLACE4000089, PLACE4000106, PLACE4000259, PLACE4000269, PLACE4000326, PLACE400 0369, PLACE4000431, PLACE4000445, PLACE4000581, PLACE4000593, PLACE4000650, PLACE40 00670,

SKNMC1000046, SKNMC1000050, SKNMC1000091, THYRO1000017, THYRO1000040, THYRO1000121, THYRO1000173, THYRO1000197, THYRO1000199, THYRO1000206, THYRO1000242, THYRO100027 0, THYRO1000288, THYRO1000320, THYRO1000327, THYRO1000358, THYRO1000394, THYRO10004 01, THYRO1000488, THYRO1000502, THYRO1000569, THYRO1000570, THYRO1000585, THYRO1000 605, THYRO1000715, THYRO1000756, THYRO1000777, THYRO1000829, THYRO1000855, THYRO100 0926, THYRO1000983, THYRO1000984, THYRO1001120, THYRO1001134, THYRO1001173, THYRO10 01204,

EXAMPLE 12

Homology search using the 5'-end and 3'-end sequences of the selected clones.

[0172] The 5' -end sequences of the selected 5547 clones were used for the homology search of the SwissProt, and both the 5' -end 3' -end sequences were used for the search of the GenBank and UniGene (ref. the result of the search of the SwissProt, GenBank (except ESTs and STSs), and UniGene (Human) was attached).

[0173] Each search result is shown in the last part of this SPECIFICATION by arranging each item in the following format.

	5' -end sequence	3' -end sequence
Swiss-Prot	Homology search result 1	-----
GenBank	Homology search result 2	Homology search result 3
UniGene	Homology search result 4	Homology search result 5

[0174] According to the top hit data, at least 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth. Among the clones predicted belonging to any of the categories, 1001 clones were estimated to have a relatively high homology with the known proteins or genes in the same category. In addition, 429 clones were estimated to have a relatively low homology with the known proteins in the same category.

[0175] Herein, the term "relatively high homology" is defined as having 60% or more identity and the P-value 10^{-10} or less in comparison with known sequences in the SwissProt database, or 64% or more identity and the P-value 10^{-15} or less in comparison with those in the GenBank and UniGene databases (see the attached list). Also, the term "relatively low homology" is defined as not fulfilling the requirements to be "relatively high homology", but still having the scores, 25% or more identity and the P-value 10^{-6} or less, using the sequence having 55 nucleotides or more, in comparison with known sequences in the SwissProt database (see the attached list). The P-value is a score obtained statistically by taking into account the probability of occurrence of the similarity between two sequences. In general, the smaller P-value reflects the higher similarity (Altschul S.F., Gish W., Miller W., Myers E.W., and Lipman D.J. (1990) "Basic local alignment search tool" J.Mol. Biol., 215: 403-410; Gish W., and States D.J. (1993) "Identification of protein coding regions by database similarity search" Nature Genet. 3: 266-272).

[0176] The clones predicted to encode a protein in the category of secretory protein or membrane protein have the keywords, "signal", "transmembrane", "membrane", "extracellular matrix", "receptor", "G-protein coupled receptor", "ionic channel", "voltage-gated channel", "calcium channel", "cell adhesion", "collagen", or "connective tissue", or descriptions from which the clone can be predicted to be a secretory or membrane protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0177] The clones predicted to encode a protein in the category of glycoprotein have the keywords, "glycoprotein", or descriptions from which the clone can be predicted to be a glycoprotein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0178] The clones predicted to encode a protein in the category of proteins associated with signal transduction have the keywords, "serine/threonine-protein kinase", "tyrosine-protein kinase", "SH3 domain", or "WD repeat", or descriptions from which the clone can be predicted to be a protein associated with signal transduction (such as "ADP-ribosylation factor"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0179] The clones predicted to encode a protein in the category of proteins associated with transcription have the keywords, "transcription regulation", "zinc finger", or "homeobox", or descriptions from which the clone can be predicted to be a protein associated with transcription, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0180] The clones predicted to encode a protein in the category of proteins associated with diseases are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein that is deposited in the Online Mendelian Inheritance in Man (OMIM) database, which is a database of human genes and diseases, or the top hit data has descriptions from which the clone can be predicted to be a protein associated with diseases.

[0181] The clones predicted to encode a protein in the category of enzyme or proteins associated with metabolism are the clones in which the top hit data of the SwissProt using the 5'-end sequence, or the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence is a gene or protein with E.C.No. (Enzyme commission number), or the top hit data has descriptions from which the clone can be predicted to be an enzyme or protein associated with metabolism (such as "metabolism", "oxidoreductase", or "lipid").

[0182] The clones predicted to encode a protein in the category of proteins associated with cell division or cell proliferation have the keywords, "cell division", "cell cycle", "mitosis", or "chromosomal protein", or descriptions from which the clone can be predicted to be a protein associated with cell division or cell proliferation (such as "histone", "cell growth", or "apoptosis"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0183] The clones predicted to encode a protein in the category of proteins associated with cytoskeleton have the keywords, "structural protein", "cytoskeleton", "actin-binding", or "microtubules", or descriptions from which the clone can be predicted to be a protein associated with cytoskeleton, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0184] The clones predicted to encode a protein in the category of proteins associated with RNA synthesis include the above clones predicted to be a protein associated with transcription, and also the clones which have the keywords, "RNA splicing", or "RNA processing", or descriptions from which the clone can be predicted to be a protein associated with RNA synthesis (such as "RNA helicase", "polyadenylation", or "RNA transport"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0185] The clones predicted to encode a protein in the category of nuclear protein include the above clones predicted to be a protein associated with transcription, and also the clones which have the keyword, "nuclear protein", or descriptions from which the clone can be predicted to be a nuclear protein, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0186] The clones predicted to encode a protein in the category of proteins associated with protein synthesis or transport have the keywords, "translation regulation", "protein biosynthesis", "amino-acid biosynthesis", "ribosomal protein", or "protein transport", or descriptions from which the clone can be predicted to be a protein associated with protein synthesis or transport (such as "signal recognition particle", "ubiquitin", "proteosome", or "protease"), in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0187] The clones predicted to encode a protein in the category of proteins associated with cellular defense have the keywords, "heat shock", "chaperone", "DNA repair", or "DNA damage", or descriptions from which the clone can be predicted to be a protein associated with cellular defense, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0188] The clones predicted to encode a protein in the category of proteins associated with development or growth have the keyword, "developmental protein", or descriptions from which the clone can be predicted to be a protein associated with development or growth, in the top hit data of the SwissProt using the 5'-end sequence, or in the top hit data of the GenBank or UniGene using the 5'-end sequence and 3'-end sequence.

[0189] The following 1430 clones were predicted to encode a protein belonging to any of the categories, secretory or membrane protein, glycoprotein, protein associated with signal transduction, protein associated with transcription, protein associated with diseases, enzyme or protein associated with metabolism, protein associated with cell division or cell proliferation, protein associated with cytoskeleton, protein associated with RNA synthesis, nuclear protein, protein associated with protein synthesis or transport, protein associated with cellular defense, or protein associated with development or growth.

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000158, HEMBA1000185, HEMBA1000201, HEMBA1000216, HEMBA1000303, HEMBA1000459, HEMBA1000488, HEMBA100049 1, HEMBA1000523, HEMBA1000531, HEMBA1000542, HEMBA1000561, HEMBA1000569, HEMBA10005 88, HEMBA1000591, HEMBA1000657, HEMBA1000673, HEMBA1000752, HEMBA1000827, HEMBA1000 851, HEMBA1000852, HEMBA1000972, HEMBA1000991, HEMBA1001017, HEMBA1001019, HEMBA100 1059, HEMBA1001071, HEMBA1001088, HEMBA1001123, HEMBA1001137, HEMBA1001174, HEMBA10 01257, HEMBA1001302, HEMBA1001351, HEMBA1001387, HEMBA1001407, HEMBA1001476, HEMBA1 001510, HEMBA1001569, HEMBA1001570, HEMBA1001579, HEMBA1001595, HEMBA1001620, HEMBA 1001672, HEMBA1001678, HEMBA1001714, HEMBA1001744, HEMBA1001800, HEMBA1001804, HEMB A1001809, HEMBA1001819, HEMBA1001822, HEMBA1001847, HEMBA1001896, HEMBA1001913, HEM BA1001921, HEMBA1002003, HEMBA1002035, HEMBA1002092, HEMBA1002102, HEMBA1002150, HE MBA1002160, HEMBA1002161, HEMBA1002162, HEMBA1002212, HEMBA1002229, HEMBA1002257, H EMBA1002341, HEMBA1002363, HEMBA1002417, HEMBA1002495, HEMBA1002513, HEMBA1002547, HEMBA1002555, HEMBA1002569, HEMBA1002609, HEMBA1002688, HEMBA1002716, HEMBA1002810, HEMBA1002896,

NT2RP2005116, NT2RP2005204, NT2RP2006565, NT2RP2006598, NT2RP3000047, NT2R P3000366, NT2RP3000759, NT2RP3000968, NT2RP3001587, NT2RP3002529, NT2RP3003385, NT2 RP3003589, NT2RP3003876, NT2RP3004618, NT2RP4000370, NT2RP4000524, NT2RP4000528, NT 2RP4001041, NT2RP4001574, NT2RP4001592, NT2RP4002047, OVARC1000004, OVARC1000771, O VARC1000862, OVARC1001180, OVARC1001342, OVARC1001766, OVARC1002138, PLACE1000061, PLACE1000492, PLACE1000863, PLACE1001748, PLACE1002090, PLACE1003394, PLACE1003915, PLACE1004149, PLACE1004743, PLACE1005557, PLACE1005813, PLACE1006488, PLACE100653 1, PLACE1006615, PLACE1007706, PLACE1008273, PLACE1008790, PLACE1008813, PLACE10097 21, PLACE1009763, PLACE1009845, PLACE1010074, PLACE1011109, PLACE1011477, PLACE2000404, PLACE3000059, PLACE3000121, PLACE4000558, PLACE4000654, SKNMC1000011, THYRO1000288, THYRO1000974, Y79AA1000346, Y79AA1000968, Y79AA1002209,

(12) The following 23 clones were predicted to encode a protein in the category of proteins associated with cellular defense (including the clones belonging to plural categories).
HEMBA1000005, HEMBA1000531, HEMBB1000217, HEMBB1000399, MAMMA1000734, NT2RP1000493, NT2RP1000493, NT2RP2000006, NT2RP2000045, NT2RP2001536, NT2RP2005204, NT2RP300059 0, NT2RP3001426, NT2RP3002056, NT2RP3004262, NT2RP4001638, OVARC1001900, PLACE10056 11, PLACE1006958, PLACE1008275, PLACE1009113, PLACE4000014, Y79AA1002139,

(13) The following 23 clones were predicted to encode a protein in the category of proteins associated with development or growth (including the clones belonging to plural categories).
HEMBB1001802, HEMBB1002442, NT2RM2002142, NT2RM4001047, NT2RP2003308, NT2RP2004816, NT2RP3000994, NT2RP3001340, NT2RP3004206, NT2RP3004472, NT2RP4000246, NT2RP400100 6, OVARC1000304, OVARC1000746, OVARC1000996, PLACE1006037, PLACE1009622, PLACE10116 64, Y79AA1001692,

Table 9

Selected clones having the maximal ATGpr1 score of 0.3 or higher (3690 clones).

clone name	name of sequence	maximal ATGpr1 score
HEMBA1000005	F-HEMBA1000005	0.84
HEMBA1000012	F-HEMBA1000012	0.56
HEMBA1000020	F-HEMBA1000020	0.94
HEMBA1000030	F-HEMBA1000030	0.44
HEMBA1000046	F-HEMBA1000046	0.50
HEMBA1000050	F-HEMBA1000050	0.94
HEMBA1000076	F-HEMBA1000076	0.48
HEMBA1000129	F-HEMBA1000129	0.74
HEMBA1000141	F-HEMBA1000141	0.55
HEMBA1000150	F-HEMBA1000150	0.72
HEMBA1000156	F-HEMBA1000156	0.94
HEMBA1000158	F-HEMBA1000158	0.62
HEMBA1000168	F-HEMBA1000168	0.94
HEMBA1000185	F-HEMBA1000185	0.86
HEMBA1000193	F-HEMBA1000193	0.94

Table 313

PLACE1005055	1.93	1.90	2.25	2.55	3.80	3.83	1.39	2.30	2.3	*	+		
PLACE1005066	3.73	3.53	2.95	3.62	2.74	3.71	4.65	6.92	6.92			*	+
PLACE1005077	1.88	0.74	0.51	1.94	2.30	1.62	1.19	1.27	1.27				
PLACE1005085	5.35	2.26	1.94	7.82	9.01	6.89	4.04	4.10	4.1	*	+		
PLACE1005086	8.18	4.09	4.61	8.82	11.72	8.88	4.94	5.91	5.91				
PLACE1005088	48.83	27.68	29.69	27.61	39.82	34.65	26.01	25.68	25.68				
PLACE1005089	2.42	1.38	1.99	2.77	2.07	2.49	2.33	3.56	3.56				
PLACE1005101	6.75	6.64	8.03	8.45	9.96	12.39	8.67	10.11	10.11			*	+
PLACE1005102	5.88	7.51	8.49	11.05	10.78	12.60	9.73	9.59	9.59	*	+	*	+
PLACE1005108	5.63	4.27	3.64	12.01	12.87	10.10	5.64	5.46	5.46	**	+		
PLACE1005110	6.84	3.16	2.29	5.61	4.42	2.27	2.47	3.96	3.96				
PLACE1005111	2.32	1.43	0.52	2.8	3.48	1.64	1.69	1.48	1.48				
PLACE1005123	20.53	8.57	10.06	12.54	14.07	10.45	7.24	8.30	8.3				
PLACE1005124	3.92	2.40	2.02	3.08	6.72	4.08	3.28	3.46	3.46				
PLACE1005128	10.6	9.42	9.74	12.9	15.61	15.03	14.09	17.89	17.89	**	+	**	+
PLACE1005130	4.63	4.42	3.58	6.21	6.12	6.60	2.90	3.62	3.62	**	+		
PLACE1005141	11.53	6.88	7.85	10.2	11.46	13.07	6.08	6.65	6.65				
PLACE1005146	2.66	2.45	2.31	3.79	4.23	2.90	1.91	2.35	2.35	*	+		
PLACE1005152	4.31	1.32	1.78	5.23	4.05	4.11	2.87	2.37	2.37				
PLACE1005157	3.17	1.71	2.58	3.61	2.97	3.04	1.83	2.24	2.24				
PLACE1005162	5.03	1.44	2.16	4.55	5.47	5.51	3.63	3.97	3.97				
PLACE1005170	1.73	0.31	0.62	1.61	1.26	1.41	1.34	1.72	1.72				
PLACE1005176	1.61	0.38	0.68	1.16	1.34	1.12	1.06	1.60	1.6				
PLACE1005181	0.5	0.24	0.53	1.19	0.87	2.59	0.77	1.26	1.26			*	+
PLACE1005184	4.44	1.78	2.90	7.9	7.10	9.09	4.75	4.64	4.64	**	+		
PLACE1005186	6.95	2.41	3.82	3.37	3.80	2.87	3.22	3.68	3.68				
PLACE1005187	3.14	1.53	1.03	3.09	5.30	4.21	2.97	2.82	2.82				
PLACE1005189	5.93	2.53	2.32	3.58	5.81	4.44	5.57	5.74	5.74				
PLACE1005193	6.13	3.49	3.63	4.29	4.51	4.47	3.64	4.00	4				
PLACE1005200	4.37	1.39	2.33	2.59	3.60	1.69	2.29	2.95	2.95				
PLACE1005206	2.34	0.51	1.37	1.54	2.19	3.01	1.80	1.98	1.98				
PLACE1005216	1.38	0.71	1.11	2.26	2.41	2.76	2.43	3.73	3.73	**	+	**	+
PLACE1005223	4.29	2.34	2.64	6.04	7.76	7.97	4.06	6.10	6.1	**	+		
PLACE1005225	19.66	8.09	9.52	16.05	21.00	13.76	8.27	9.44	9.44				
PLACE1005232	8.02	4.04	2.69	6.94	10.56	7.61	5.96	6.58	6.58				
PLACE1005239	5.38	1.20	2.07	5.01	3.78	2.93	2.36	3.31	3.31				
PLACE1005243	5.32	3.76	4.72	5.19	5.09	5.33	3.34	5.82	5.82				
PLACE1005250	3.75	1.12	1.85	3.16	3.89	3.16	2.16	2.84	2.84				
PLACE1005261	2.07	0.70	1.90	2.25	2.05	1.77	2.13	1.93	1.93				
PLACE1005266	1.9	0.95	1.09	2.57	2.39	2.64	2.14	1.90	1.9	*	+		
PLACE1005271	5.66	2.63	3.94	8.71	9.11	8.37	4.71	5.02	5.02	**	+		
PLACE1005277	3.05	0.82	0.70	2.46	4.32	1.50	1.02	2.07	2.07				
PLACE1005287	6.59	3.30	3.94	10.35	15.42	7.57	8.69	8.45	8.45			*	+
PLACE1005299	22.18	11.98	9.53	18.56	24.11	17.96	21.90	22.45	22.45				
PLACE1005305	5.96	2.44	4.52	8.17	10.96	9.42	8.88	11.22	11.22	*	+	**	+
PLACE1005307	3.74	1.42	2.86	4.85	5.32	3.53	2.69	4.11	4.11				
PLACE1005308	3.94	1.81	2.45	3.16	2.71	2.64	2.67	2.60	2.6				
PLACE1005313	1.8	1.22	2.93	1.89	0.89	2.76	1.70	1.69	1.69				
PLACE1005320	2.05	0.78	1.58	1.96	1.63	3.04	1.42	1.54	1.54				
PLACE1005327	3.57	2.45	2.12	2.64	6.29	3.81	4.41	6.45	6.45			*	+
PLACE1005331	4	2.27	3.11	3.34	6.04	3.03	3.28	2.86	2.86				
PLACE1005335	9.31	5.05	4.18	8.68	7.24	5.98	5.53	6.95	6.95				
PLACE1005336	3.13	1.45	2.61	5.52	6.69	4.80	4.00	4.81	4.81	*	+	*	+
PLACE1005351	30.75	16.28	19.31	14.85	14.56	18.13	32.39	30.68	30.68				
PLACE1005366	3.38	2.74	2.56	10.21	9.37	10.62	9.15	9.50	9.5	**	+	**	+
PLACE1005373	4.26	1.58	2.70	3.39	2.69	4.82	2.63	3.29	3.29				

PLACE1004736	F-PLACE1004736	0.80
PLACE1004740	F-PLACE1004740	0.34
PLACE1004743	F-PLACE1004743	0.70
PLACE1004751	F-PLACE1004751	0.49
PLACE1004777	F-PLACE1004777	0.72
PLACE1004804	F-PLACE1004804	0.46
PLACE1004814	F-PLACE1004814	0.70
PLACE1004824	F-PLACE1004824	0.63
PLACE1004868	F-PLACE1004868	0.94
PLACE1004885	F-PLACE1004885	0.63
PLACE1004902	F-PLACE1004902	0.56
PLACE1004918	F-PLACE1004918	0.85
PLACE1004930	F-PLACE1004930	0.83
PLACE1004937	F-PLACE1004937	0.46
PLACE1004969	F-PLACE1004969	0.62
PLACE1004982	F-PLACE1004982	0.61
PLACE1005026	F-PLACE1005026	0.81
PLACE1005027	F-PLACE1005027	0.91
PLACE1005046	F-PLACE1005046	0.31
PLACE1005055	F-PLACE1005055	0.57
PLACE1005066	F-PLACE1005066	0.68
PLACE1005101	F-PLACE1005101	0.94
PLACE1005102	F-PLACE1005102	0.94
PLACE1005181	F-PLACE1005181	0.94
PLACE1005187	F-PLACE1005187	0.94
PLACE1005206	F-PLACE1005206	0.67
PLACE1005232	F-PLACE1005232	0.72
PLACE1005243	F-PLACE1005243	0.81
PLACE1005261	F-PLACE1005261	0.75
PLACE1005266	F-PLACE1005266	0.55
PLACE1005277	F-PLACE1005277	0.43
PLACE1005287	F-PLACE1005287	0.77
PLACE1005305	F-PLACE1005305	0.94
PLACE1005308	F-PLACE1005308	0.46
PLACE1005313	F-PLACE1005313	0.94
PLACE1005327	F-PLACE1005327	0.82
PLACE1005331	F-PLACE1005331	0.94
PLACE1005335	F-PLACE1005335	0.94
PLACE1005373	F-PLACE1005373	0.71
PLACE1005374	F-PLACE1005374	0.82
PLACE1005480	F-PLACE1005480	0.43
PLACE1005481	F-PLACE1005481	0.42
PLACE1005494	F-PLACE1005494	0.34
PLACE1005530	F-PLACE1005530	0.94
PLACE1005550	F-PLACE1005550	0.86
PLACE1005554	F-PLACE1005554	0.34

PLACE1003256, PLACE1003361, PLACE1003493, PLACE1003519, PLACE1003528, PLACE1003566, PLACE1003592, PLACE1003870, PLACE1003968, PLACE1004103, PLACE1004149, PLACE1004156, PLACE1004161, PLACE1004242, PLACE1004336, PLACE1004358, PLACE1004672, PLACE1004736, PLACE1004824, PLACE1004900, PLACE1004979, PLACE1005086, PLACE1005101, PLACE1005102, PLACE1005128, PLACE1005232, PLACE1005528, PLACE1006002, PLACE1006139, PLACE1006412, PLACE1006540, PLACE1007132, PLACE1007367, PLACE1008405, PLACE1008457, PLACE1010310, PLACE1011056, PLACE1011340, PLACE1011646, PLACE1011783, PLACE2000003, PLACE2000030, PLACE2000039, PLACE2000047, PLACE2000124, PLACE2000235, PLACE2000305, PLACE2000335, PLACE2000347, PLACE2000411, PLACE2000419, PLACE2000435, PLACE2000450, PLACE2000465, PLACE3000004, PLACE3000009, PLACE3000070, PLACE3000124, PLACE3000136, PLACE3000145, PLACE3000155, PLACE3000158, PLACE3000207, PLACE3000254, PLACE3000271, PLACE3000304, PLACE3000331, PLACE3000399, PLACE3000401, PLACE3000455, PLACE3000475, PLACE4000009, PLACE4000049, PLACE4000128, PLACE4000131, PLACE4000192, PLACE4000211, PLACE4000250, PLACE4000323, PLACE4000445, PLACE4000450, PLACE4000465, PLACE4000612, THYR01000085, THYR01000132, THYR01000186, THYR01000484, THYR01000569, THYR01000699, THYR01000712, THYR01000815, THYR01001173, THYR01001189, THYR01001401, THYR01001406, THYR01001411, THYR01001426, THYR01001480, THYR01001487, THYR01001537, THYR01001637, THYR01001772, THYR01001793, THYR01001828, THYR01001854, Y79AA1000059, Y79AA1000131, Y79AA1000202, Y79AA1000214, Y79AA1000231, Y79AA1000313, Y79AA1000342, Y79AA1000349, Y79AA1000410, Y79AA1000539, Y79AA1000560, Y79AA1000589, Y79AA1000833, Y79AA1000985, Y79AA1001077, Y79AA1001145, Y79AA1001216, Y79AA1001228, Y79AA1001299, Y79AA1001402, Y79AA1001548, Y79AA1001603, Y79AA1001613, Y79AA1001805, Y79AA1002472, Y79AA1002482.

[0203] Genes that were expressed at low levels in any of the tissues tested are indicated below by the corresponding clone names:

OVARC1002156, PLACE1000005, PLACE1000040, PLACE1000048, PLACE1000133,
PLACE1000184, PLACE1000214, PLACE1000308, PLACE1000332, PLACE1000380,
PLACE1000383, PLACE1000540, PLACE1000636, PLACE1000653, PLACE1000716,
PLACE1000748, PLACE1000755, PLACE1000769, PLACE1000841, PLACE1000856,
PLACE1000909, PLACE1000977, PLACE1001000, PLACE1001010, PLACE1001015,
PLACE1001076, PLACE1001088, PLACE1001168, PLACE1001171, PLACE1001241,
PLACE1001279, PLACE1001294, PLACE1001351, PLACE1001377, PLACE1001383,
PLACE1001384, PLACE1001395, PLACE1001412, PLACE1001468, PLACE1001534,
PLACE1001551, PLACE1001602, PLACE1001634, PLACE1001716, PLACE1001771,
PLACE1001781, PLACE1001810, PLACE1001817, PLACE1001844, PLACE1001845,
PLACE1001920, PLACE1001928, PLACE1002052, PLACE1002115, PLACE1002150,
PLACE1002171, PLACE1002205, PLACE1002256, PLACE1002259, PLACE1002319,
PLACE1002399, PLACE1002438, PLACE1002450, PLACE1002493, PLACE1002499,
PLACE1002529, PLACE1002571, PLACE1002583, PLACE1002591, PLACE1002598,
PLACE1002625, PLACE1002768, PLACE1002772, PLACE1002782, PLACE1002794,
PLACE1002815, PLACE1002839, PLACE1002851, PLACE1002853, PLACE1002908,
PLACE1002962, PLACE1002996, PLACE1003027, PLACE1003044, PLACE1003045,
PLACE1003092, PLACE1003145, PLACE1003174, PLACE1003176, PLACE1003190,
PLACE1003200, PLACE1003238, PLACE1003258, PLACE1003334, PLACE1003343,
PLACE1003375, PLACE1003383, PLACE1003401, PLACE1003516, PLACE1003521,
PLACE1003537, PLACE1003583, PLACE1003593, PLACE1003602, PLACE1003618,
PLACE1003625, PLACE1003669, PLACE1003709, PLACE1003771, PLACE1003783,
PLACE1003784, PLACE1003864, PLACE1003888, PLACE1003892, PLACE1003915,
PLACE1003923, PLACE1003932, PLACE1004118, PLACE1004197, PLACE1004257,
PLACE1004258, PLACE1004274, PLACE1004284, PLACE1004302, PLACE1004316,
PLACE1004388, PLACE1004405, PLACE1004425, PLACE1004451, PLACE1004460,
PLACE1004473, PLACE1004491, PLACE1004516, PLACE1004550, PLACE1004664,
PLACE1004674, PLACE1004693, PLACE1004716, PLACE1004722, PLACE1004777,
PLACE1004793, PLACE1004813, PLACE1004815, PLACE1004827, PLACE1004836,
PLACE1004840, PLACE1004868, PLACE1004913, PLACE1004918, PLACE1004930,
PLACE1004969, PLACE1004972, PLACE1004985, PLACE1005026, PLACE1005055,
PLACE1005077, PLACE1005162, PLACE1005176, PLACE1005181, PLACE1005187,
PLACE1005206, PLACE1005261, PLACE1005266, PLACE1005287, PLACE1005313,
PLACE1005471, PLACE1005480, PLACE1005481, PLACE1005494, PLACE1005502,
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OVARC1001038, OVARC1001055, OVARC1001085, OVARC1001129, OVARC1001167, OVARC1001339, OVARC1001425, OVARC1001745, OVARC1001762, OVARC1001766, OVARC1001942, OVARC1002044, OVARC1002138, PLACE1000004, PLACE1000005, PLACE1000420, PLACE1000547, PLACE1000562, PLACE1000653, PLACE1001168, PLACE1001311, PLACE1001377, PLACE1001920, PLACE1001983, PLACE1002066, PLACE1002072, PLACE1002140, PLACE1002171, PLACE1002319, PLACE1002474, PLACE1002499, PLACE1002532, PLACE1002665, PLACE1003025, PLACE1003145, PLACE1003361, PLACE1003605, PLACE1003704, PLACE1003783, PLACE1003885, PLACE1004405, PLACE1004629, PLACE1004686, PLACE1004930, PLACE1005066, PLACE1006077, PLACE1005630, PLACE1005876, PLACE1006143, PLACE1006325, PLACE1006488, PLACE1006805, PLACE1006829, PLACE1007286, PLACE1007858, PLACE1008201, PLACE1009045, PLACE1009113, PLACE1009621, PLACE1010106, PLACE1010310, PLACE1010622, PLACE1010944, PLACE1010965, PLACE1011185, PLACE1011332, PLACE1011635, PLACE1011646, PLACE1011725, PLACE2000014, PLACE2000264, PLACE2000394, PLACE2000419, PLACE3000160, PLACE3000220, PLACE3000254, PLACE3000271, PLACE3000339, PLACE3000341, PLACE3000350, PLACE3000353, PLACE3000401, PLACE4000300, SKNMC1000091, THYRO1000855, THYRO1001559, Y79AA1000065, Y79AA1000202, Y79AA1000214, Y79AA1000346, Y79AA1000784, Y79AA1000833, Y79AA1000968, Y79AA1001555, Y79AA1002220.

[0235] Clones of which expression levels decrease by TNF-α are as follows:

HEMBA1002150, HEMBB1000240, NT2RM2000469, NT2RM2000984, NT2RM2001688, NT2RM4000290, NT2RM4000496, NT2RM4000590, NT2RM4001047, NT2RM4001582, NT2RM4001611, NT2RM4001650, NT2RM4002075, NT2RM4002128, NT2RP1000174, NT2RP1000243, NT2RP1000581, NT2RP1000688, NT2RP1000767, NT2RP1000825, NT2RP1001185, NT2RP1001286, NT2RP1001432, NT2RP1001457, NT2RP2000001, NT2RP2000248, NT2RP2000841, NT2RP2001813, NT2RP2002137, NT2RP2002928, NT2RP2003517, NT2RP2003559, NT2RP2003564, NT2RP2004933, NT2RP2005038, NT2RP2006365, NT2RP3000072, NT2RP3000320, NT2RP3000484, NT2RP3000980, NT2RP3001111, NT2RP3001420, NT2RP3001495, NT2RP3002056, NT2RP3002057, NT2RP3002545, NT2RP3002713, NT2RP3002799, NT2RP3002869, NT2RP3002953, NT2RP3002955, NT2RP3003282, NT2RP3003290, NT2RP3003384, NT2RP3003385, NT2RP3003870, NT2RP3004207, NT2RP3004262, NT2RP3004527, NT2RP4000500, NT2RP4000524, NT2RP4000787, NT2RP4000927, NT2RP4000955, NT2RP4000989, NT2RP4001442, NT2RP4001638, NT2RP4001950, NT2RP4002888, NT2RP5003524, OVARC1001270, PLACE1000246, PLACE1002816.

[0236] These are rheumatoid arthritis-associated clones.

Analysis of ultraviolet radiation damage-associated genes

[0237] It is known that ultraviolet rays give considerably adverse influence on the health. In recent years, there have been significant risks of tissue damage by ultraviolet rays because of destruction of the ozone layer. Thus, ultraviolet radiation has been recognized as a risk factor for skin diseases such as skin cancers (United States Environmental Protection Agency: Ozone Depletion Home Page, http://www.epa.gov/ozone/). Genes of which expression levels are varied in skin epidermal cells exposed to ultraviolet rays are considered to be associated with skin damage caused by ultraviolet radiation.

[0238] After primary cultured skin fibroblast cells were irradiated with ultraviolet ray and were cultured, a survey was performed for genes of which expression levels were varied depending on the irradiation of ultraviolet ray. First, after cultured to be confluent, the primary cultured skin fibroblast cells (Cell Applications) were exposed to 10,000 $\mu J/cm^2$ of 254-nm ultraviolet light.

[0239] Messenger RNAs were, then, extracted by using a FastTrack™ 2.0 mRNA Isolation kit (Invitrogen Co.) from the unexposed cells and from the cells that were exposed to the ultraviolet light and then cultured for 4 or 24 hours. The labeling of the hybridization probe was carried out by using a 1.5 μg of each mRNA in the same manner as described above. The data were obtained in triplicate (n=3). The hybridization signals were compared between the cells exposed to the ultraviolet light and the unexposed cells. The comparison was preformed by statistical treatment with two-sample t-test. Clones with significant differences in the signal distribution were selected under the condition of $p<0.05$. In this analysis, even when the signal is lower than others, the difference in the signal values can be detected statistically. Accordingly, clones with signal value of 40 or lower were also assessed for selection.

[0240] Tables 353-509 show the expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light.

[0241] Averaged signal values (M_1, M_2) and sample variances (s_1^2, s_2^2) were calculated for each gene in each of the cells, and then, the pooled sample variances s^2 were obtained from the sample variances of the two types of cells to be compared. The t values were determined according to the following formula: $t=(M_1-M_2)/s/(1/3+1/3)^{1/2}$. When the determined t-value was greater than a t-value at P, which means the probability of significance level, of 0.05 or 0.01

in the t-distribution table with 4 degrees of freedom, the difference was judged to be found in the expression level of the gene between the two types of cells at $p<0.05$ or $p<0.01$, respectively. The tables also include the information of an increase (+) or decrease (-) in the expression level of a gene in the exposed cells in comparison with that of unexposed cells.

[0242] The expression levels of the following clones were elevated 4 or 24 hours after the ultraviolet irradiation:
HEMBA1000542, HEMBA1001808, HEMBA1002177, HEMBA1003314, MAMMA1001874, NT2RM2001100, NT2RP2005732, NT2RP3000592, NT2RP4000657, OVARC1000004, OVARC1001092, OVARC1001342, PLACE1002816, NT2RM4001002, NT2RM4001813, NT2RM4002266, NT2RP2001174, NT2RP2001196, NT2RP2005358, NT2RP3000690, NT2RP3001216, NT2RP3003464, PLACE1006382, THYRO1000070, THYRO1001100, Y79AA1000342.

[0243] The expression levels of the following clones were decreased 4 or 24 hours after the ultraviolet irradiation:
HEMBA1000005, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000231, HEMBA1000304, HEMBA1000307, HEMBA1000333, HEMBA1000366, HEMBA1000369, HEMBA1000390, HEMBA1000396, HEMBA1000418, HEMBA1000434, HEMBA1000464, HEMBA1000469, HEMBA1000490, HEMBA1000504, HEMBA1000505, HEMBA1000557, HEMBA1000657, HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000727, HEMBA1000752, HEMBA1000851, HEMBA1000852, HEMBA1000870, HEMBA1000872, HEMBA1001085, HEMBA1001121, HEMBA1001133, HEMBA1001235, HEMBA1001265, HEMBA1001281, HEMBA1001289, HEMBA1001299, HEMBA1001303, HEMBA1001310, HEMBA1001323, HEMBA1001595, HEMBA1001620, HEMBA1001640, HEMBA1001678, HEMBA1001712, HEMBA1001835, HEMBA1001950, HEMBA1001987, HEMBA1002253, HEMBA1002321, HEMBA1002341, HEMBA1002419, HEMBA1002679, HEMBA1002728, HEMBA1002818, HEMBA1002935, HEMBA1002999, HEMBA1003034, HEMBA1003071, HEMBA1003098, HEMBA1003142, HEMBA1003175, HEMBA1003202, HEMBA1003212, HEMBA1003220, HEMBA1003276, HEMBA1003373, HEMBA1003417, HEMBA1003447, HEMBA1003528, HEMBA1003684, HEMBA1003799, HEMBA1003885, HEMBA1003989, HEMBA1004011, HEMBA1004055, HEMBA1004133, HEMBA1004225, HEMBA1004272, HEMBA1004353, HEMBA1004631, HEMBA1004669, HEMBA1004705, HEMBA1004753, HEMBA1004776, HEMBA1004803, HEMBA1004816, HEMBA1004900, HEMBA1005047, HEMBA1005079, HEMBA1005101, HEMBA1005149, HEMBA1005152, HEMBA1005202, HEMBA1005314, HEMBA1005372, HEMBA1005511, HEMBA1005513, HEMBA1005518, HEMBA1005570, HEMBA1005577, HEMBA1005581, HEMBA1005588, HEMBA1005609, HEMBA1005632, HEMBA1005853, HEMBA1006031, HEMBA1006035, HEMBA1006485, HEMBA1006486, HEMBA1006502, HEMBA1006696, HEMBA1006789, HEMBA1006796, HEMBA1007085, HEMBA1007224, HEMBA1007301, HEMBA1007319, HEMBA1007341, HEMBA1007342, HEMBB1000036, HEMBB1000037, HEMBB1000217, HEMBB1000266, HEMBB1000317, HEMBB1000336, HEMBB1000354, HEMBB1000369, HEMBB1000399, HEMBB1000434, HEMBB1000438, HEMBB1000592, HEMBB1000673, HEMBB1000789, HEMBB1000810, HEMBB1000883, HEMBB1000887, HEMBB1001105, HEMBB1001182, HEMBB1001242, HEMBB1001267, HEMBB1001424, HEMBB1001464, HEMBB1001531, HEMBB1001618, HEMBB1001996, HEMBB1002092, HEMBB1002139, HEMBB1002142, HEMBB1002190, HEMBB1002453, HEMBB1002520, HEMBB1002550, HEMBB1002556, HEMBB1002600, HEMBB1002664, MAMMA1000009, MAMMA1000055, MAMMA1000069, MAMMA1000133, MAMMA1000171, MAMMA1000173, MAMMA1000287, MAMMA1000416, MAMMA1000585, MAMMA1000713, MAMMA1000760, MAMMA1000798, MAMMA1000831, MAMMA1000875, MAMMA1000876, MAMMA1000877, MAMMA1000906, MAMMA1000931, MAMMA1000962, MAMMA1001133, MAMMA1001139, MAMMA1001243, MAMMA1001271, MAMMA1001274, MAMMA1001298, MAMMA1001606, MAMMA1001630, MAMMA1001670, MAMMA1001743, MAMMA1001751, MAMMA1002140, MAMMA1002145, MAMMA1002158, MAMMA1002170, MAMMA1002236, MAMMA1002311, MAMMA1002498, MAMMA1002754, MAMMA1002780, MAMMA1002820, MAMMA1002843, MAMMA1002844, MAMMA1002871, MAMMA1003047, NT2RM1000037, NT2RM1000039, NT2RM1000080, NT2RM1000086, NT2RM1000341, NT2RM1000499, NT2RM1000669, NT2RM1000746, NT2RM1000781, NT2RM1000885, NT2RM1000905, NT2RM1000962, NT2RM2000239, NT2RM2000260, NT2RM2000371, NT2RM2000639, NT2RM2000649, NT2RM2000735, NT2RM2000821, NT2RM2000984, NT2RM2001035, NT2RM2001065, NT2RM2001105, NT2RM2001177, NT2RM2001194, NT2RM2001196, NT2RM2001243, NT2RM2001256, NT2RM2001424, NT2RM2001588, NT2RM2001635, NT2RM2001648, NT2RM2001652, NT2RM2001668, NT2RM2001706, NT2RM2001727, NT2RM2001730, NT2RM2001743, NT2RM2001753, NT2RM2001760, NT2RM2001771, NT2RM2001785, NT2RM2001800, NT2RM2001855, NT2RM2001896, NT2RM2001997, NT2RM2002030, NT2RM2002049, NT2RM2002091, NT2RM2002142, NT2RM2002145, NT2RM2002178, NT2RM2002580, NT2RM4000215, NT2RM4000344, NT2RM4000368, NT2RM4000421, NT2RM4000425, NT2RM4000457, NT2RM4000496, NT2RM4000515, NT2RM4000712, NT2RM4000787, NT2RM4000813, NT2RM4000820, NT2RM4000852, NT2RM4000950, NT2RM4000996, NT2RM4001016, NT2RM4001047, NT2RM4001054, NT2RM4001140, NT2RM4001151, NT2RM4001187, NT2RM4001204, NT2RM4001258, NT2RM4001437, NT2RM4001454, NT2RM4001489, NT2RM4001605,

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[0244] These clones are ultraviolet radiation damage-associated clones.

Table 12

Expression of each cDNA in human tissues (containing clones that are not described in Examples.)

Table 137

PLACE1005027	96.103	120.663	38.137	45.870	39.089	34.870	44.104	36.457
PLACE1005031	53.784	60.972	22.926	20.892	23.652	30.271	33.677	36.405
PLACE1005036	59.627	65.001	32.797	39.527	17.608	26.473	31.634	38.146
PLACE1005041	4.201	12.290	6.164	5.522	7.108	4.000	7.035	4.518
PLACE1005046	87.532	76.016	48.856	61.696	38.790	39.618	40.595	41.016
PLACE1005047	46.051	25.735	13.704	11.855	15.156	16.153	36.409	23.815
PLACE1005052	46.575	28.140	12.015	12.780	14.059	19.834	31.197	29.860
PLACE1005055	8.158	27.571	18.813	20.078	22.643	10.820	20.439	26.659
PLACE1005066	42.175	53.415	23.566	15.565	25.138	25.274	51.837	39.544
PLACE1005077	24.309	28.659	13.050	14.623	12.679	15.734	21.504	21.488
PLACE1005085	92.222	93.468	34.255	47.138	34.582	40.497	36.256	38.289
PLACE1005086	102.289	115.876	53.702	57.228	50.800	42.000	46.257	54.679
PLACE1005088	544.154	104.456	118.967	73.371	168.988	196.566	151.442	82.439
PLACE1005089	15.670	20.631	11.122	11.637	9.823	8.077	15.337	12.098
PLACE1005101	240.793	118.635	90.799	64.835	74.093	133.434	208.569	89.985
PLACE1005102	211.056	131.745	94.963	67.285	83.058	115.827	185.343	115.880
PLACE1005108	106.691	120.848	45.131	39.846	39.785	42.063	67.557	51.335
PLACE1005110	44.564	38.347	24.937	14.829	19.447	30.115	34.784	22.848
PLACE1005111	23.753	40.474	14.465	9.594	18.283	14.066	20.594	18.691
PLACE1005123	59.496	91.632	49.521	37.074	43.380	35.861	40.754	46.181
PLACE1005124	40.401	51.742	18.340	18.486	14.709	15.681	58.570	27.105
PLACE1005128	204.940	150.075	112.018	69.631	91.526	103.298	146.254	123.511
PLACE1005130	60.815	73.959	31.043	64.232	33.067	33.874	55.788	78.228
PLACE1005141	31.384	66.806	13.194	14.252	14.502	14.628	19.090	38.173
PLACE1005146	41.144	50.277	22.100	13.293	17.449	21.199	50.528	27.607
PLACE1005152	24.085	22.701	12.226	17.968	9.903	11.357	15.172	18.599
PLACE1005157	12.965	19.465	14.891	8.624	4.456	13.395	11.532	13.083
PLACE1005162	36.700	33.286	16.285	22.399	12.111	12.771	17.199	19.584
PLACE1005170	10.498	22.471	9.375	11.193	6.555	8.512	31.001	12.095
PLACE1005176	14.622	9.067	7.477	7.780	4.490	12.946	17.364	10.281
PLACE1005181	6.793	9.688	13.589	5.174	11.314	5.046	10.911	5.455
PLACE1005184	45.108	51.852	28.259	28.577	14.895	17.723	18.400	25.953
PLACE1005186	44.227	18.348	9.815	8.521	7.622	25.120	58.044	15.795
PLACE1005187	35.399	20.464	13.526	17.276	12.357	24.314	23.687	19.988
PLACE1005189	22.364	32.597	20.000	13.876	11.241	20.988	33.066	19.839
PLACE1005193	49.047	60.518	24.364	25.042	13.468	27.467	43.397	28.759
PLACE1005200	33.619	67.147	18.122	26.564	10.723	25.057	36.262	35.781
PLACE1005206	7.546	16.382	8.064	9.582	7.561	2.781	8.835	9.588
PLACE1005216	12.005	12.262	6.329	7.983	11.377	8.113	19.335	10.996
PLACE1005223	61.568	52.800	42.403	50.792	22.094	32.500	31.112	40.207
PLACE1005225	56.429	68.319	36.647	41.380	13.973	38.303	34.273	28.689
PLACE1005232	167.040	125.455	69.019	54.944	48.079	58.072	51.258	47.854
PLACE1005239	39.974	13.868	24.220	12.450	8.314	22.398	17.024	10.214
PLACE1005243	44.314	40.194	24.574	15.713	15.164	30.409	32.149	27.769
PLACE1005250	16.580	27.491	8.463	9.418	9.886	6.064	14.623	19.833
PLACE1005261	13.408	16.822	8.222	5.682	5.972	7.195	10.054	11.287
PLACE1005266	20.535	27.721	31.380	28.026	16.734	16.639	19.888	14.312
PLACE1005271	93.263	83.479	52.747	61.756	25.077	54.250	44.786	57.870
PLACE1005277	49.402	22.460	14.621	13.425	7.075	14.242	10.306	12.244
PLACE1005287	22.199	38.345	37.586	27.355	20.932	23.076	24.235	32.916
PLACE1005299	103.926	106.254	44.038	32.012	31.443	51.044	46.947	40.737
PLACE1005305	31.910	44.987	25.573	14.702	9.928	36.933	23.937	7.784
PLACE1005307	8.172	12.030	16.098	3.745	9.584	6.781	7.722	11.443
PLACE1005308	40.902	25.016	19.027	14.696	9.927	17.505	29.543	18.123
PLACE1005313	39.342	24.175	12.571	9.132	10.374	15.637	19.991	21.756
PLACE1005320	11.271	17.455	5.231	8.538	6.936	8.957	11.506	3.500
PLACE1005327	17.688	40.290	17.575	16.817	11.658	12.028	22.217	11.328
PLACE1005331	53.315	18.698	8.600	7.329	10.301	14.685	21.018	30.181
PLACE1005335	77.870	63.026	41.750	23.138	24.128	41.168	47.208	30.379
PLACE1005336	21.324	20.435	19.530	20.249	15.524	17.918	9.870	18.733
PLACE1005351	322.456	95.522	98.703	40.129	88.620	198.287	224.069	67.745
PLACE1005366	43.968	40.039	29.574	12.918	26.291	12.458	22.106	17.170
PLACE1005373	45.621	33.656	36.861	29.023	24.691	30.472	35.702	32.653
PLACE1005374	65.634	77.534	33.162	35.300	28.763	35.173	31.282	34.469

Expression of each cDNA in human pulmonary arterial endothelial cells cultured in a medium containing bovine serum albumin, glycosylated bovine serum albumin or advanced glycosylated endproduct of bovine serum albumin (This table also contains clones with no description in Examples).

In the table, EC_G_B/EC_BSA and EC_A_B/EC_BSA represent ratios of EC_glycated_BSA/EC_BSA and EC_AGE_BSA/EC_BSA, respectively.

Clone_name	EC_BSA	EC_glycated_BSA	EC_AGE_BSA	EC_G_B /EC_BSA	EC_A_B /EC_BSA
GAPDH(Cr1)	100.81	134.21	115.16	1.33	1.14
β actin(Cr2)	1101.9	1092.57	997.36	0.99	0.91
ADRGL1000005	26.88	38.27	36.13	1	1
ADRGL1000007	117.89	127.25	133.21	1.08	1.13
ADRGL1000009	29.18	25.65	26.05	1	1
ADRGL1000011	88.9	117.33	142.9	1.32	1.61
ADRGL1000027	33.24	40.53	43.02	1.01	1.08
ADRGL1000058	153.41	208.84	180.05	1.36	1.17
ADRGL1000069	16.8	21.77	29.81	1	1
ADRGL1000077	25.74	24.72	32.86	1	1
ADRGL1000092	84.52	84.15	121.76	1	1.44
ADRGL1000099	76.19	91.53	106.01	1.2	1.39
ADRGL1000136	52.34	44.76	63.06	0.86	1.2
ADRGL1000147	46.08	45.18	52.15	0.98	1.13
ADRGL1000159	31.52	40.24	42.72	1.01	1.07
ADRGL1000160	52.34	60.37	62.29	1.15	1.19
ADRGL1000171	21.46	16.78	25.59	1	1
ADRGL1000181	37.44	45.71	43.65	1.14	1.09
BGGI11000015	52.42	71	65.47	1.35	1.25
BGGI11000016	127.44	122.93	147.57	0.96	1.16
BGGI11000017	25.65	25.74	31.33	1	1
BGGI11000022	32.82	35.19	25.56	1	1
BGGI11000031	44.42	43.8	40.25	0.99	0.91
BGGI11000042	120.38	146.44	165.42	1.22	1.37
BGGI11000046	74.72	58.85	84.95	0.79	1.14
BNGH41000020	4286.0	3584.67	4330.96	0.84	1.01
BNGH41000025	216.67	223.74	257.06	1.03	1.19
BNGH41000026	25.76	28.16	35.52	1	1
BNGH41000027	29.23	23.83	17.86	1	1
BNGH41000035	280.32	238.34	305.66	0.85	1.09
BNGH41000037	59.14	54.86	54.58	0.93	0.92
BNGH41000042	356.1	324.08	411.07	0.91	1.15
BNGH41000048	1201.3	869.03	739.91	0.72	0.62
BNGH41000056	33.94	31.4	40.01	1	1
BNGH41000087	77.58	81.76	91.07	1.05	1.17
BNGH41000091	21.05	21.23	26.82	1	1

PLACE1005250	63.7	64.27	69.23	1.01	1.09
PLACE1005261	39.94	47.49	45.93	1.19	1.15
PLACE1005266	50.13	47.62	41.62	0.95	0.83
PLACE1005271	105.46	119.85	107.51	1.14	1.02
PLACE1005277	23.12	23.98	23.79	1	1
PLACE1005287	34.49	30.55	24.59	1	1
PLACE1005299	227.75	244.53	240.7	1.07	1.06
PLACE1005305	69.35	58.03	70.36	0.84	1.01
PLACE1005307	47.35	45	36.3	0.95	0.84
PLACE1005308	69.41	60.66	61.59	0.87	0.89
PLACE1005313	30.06	30.16	21.98	1	1
PLACE1005320	23.98	27.05	34.24	1	1
PLACE1005327	115.46	121.53	98.08	1.05	0.85
PLACE1005331	30.68	23.63	27.98	1	1
PLACE1005335	21.07	19.09	21.14	1	1
PLACE1005336	59.36	64.07	46.08	1.08	0.78
PLACE1005351	214.19	250.8	232.92	1.17	1.09
PLACE1005366	40.76	25.34	38.17	0.98	0.98
PLACE1005373	39.99	49.78	40.8	1.24	1.02
PLACE1005374	72.3	70.1	60.1	0.97	0.83
PLACE1005383	28.31	37.28	28.35	1	1
PLACE1005388	20.09	15.33	18.44	1	1
PLACE1005409	41.93	44.79	33.57	1.07	0.95
PLACE1005410	88.35	94.3	106.85	1.07	1.21
PLACE1005426	19.09	18.98	20.59	1	1
PLACE1005431	88.69	108.82	135.42	1.23	1.53
PLACE1005453	71.2	88.48	54.16	1.24	0.76
PLACE1005467	77.47	67.27	64.65	0.87	0.83
PLACE1005471	25.1	22.55	17.51	1	1
PLACE1005476	18.71	20.07	18.3	1	1
PLACE1005477	41.23	32.25	32.73	0.97	0.97
PLACE1005480	17.77	14.42	12.46	1	1
PLACE1005481	50.84	54.24	40.04	1.07	0.79
PLACE1005494	20.43	21.23	13.29	1	1
PLACE1005495	40.63	117.46	154.7	2.89	3.81
PLACE1005497	42.63	75.44	65.24	1.77	1.53
PLACE1005499	80.45	84.52	88.63	1.05	1.1
PLACE1005502	27.31	28.42	23.04	1	1
PLACE1005513	23.38	27.63	25.62	1	1
PLACE1005515	17.68	23.24	12.33	1	1
PLACE1005519	52.35	24.62	32.27	0.76	0.76
PLACE1005526	20.49	19.76	12.62	1	1
PLACE1005528	99.57	107.34	90.46	1.08	0.91
PLACE1005530	107.92	99.06	99.36	0.92	0.92
PLACE1005536	27.52	29.04	23.69	1	1
PLACE1005539	22.2	17.91	26.37	1	1

Y79AA1002355	48.88	42.39	40.68	0.87	0.83
Y79AA1002361	87.11	88.66	76.9	1.02	0.88
Y79AA1002365	38.75	24.26	20.53	1	1
Y79AA1002373	43.96	55.06	28.34	1.25	0.91
Y79AA1002376	3080.7	3824.05	4481.1	1.24	1.45
Y79AA1002378	73.33	93.61	68.22	1.28	0.93
Y79AA1002381	248.36	288.51	304.13	1.16	1.22
Y79AA1002388	118.82	135.82	129.37	1.14	1.09
Y79AA1002399	36.12	30.1	32.87	1	1
Y79AA1002407	57.84	42.82	52.54	0.74	0.91
Y79AA1002413	78.77	81.36	87.31	1.03	1.11
Y79AA1002416	34.3	30.2	51.99	1	1.3
Y79AA1002429	67.91	69.81	80.19	1.03	1.18
Y79AA1002431	24.66	21.16	23.98	1	1
Y79AA1002433	27.12	18.11	23.63	1	1
Y79AA1002445	78.66	54.58	73.75	0.69	0.94
Y79AA1002461	29.04	24.84	32	1	1
Y79AA1002466	882.69	904.65	782.53	1.02	0.89
Y79AA1002471	53.74	51.26	68.91	0.95	1.28
Y79AA1002472	121.95	127.4	127.11	1.04	1.04
Y79AA1002474	53.33	40.85	47.18	0.77	0.88
Y79AA1002482	103.36	111.11	116.07	1.07	1.12
Y79AA1002487	30.92	25.8	32.51	1	1
Y79AA1002490	101.4	90.92	90.54	0.9	0.89
Y79AA1002493	107.88	125.54	105.75	1.16	0.98
ZRV6C1006278	46.63	30.08	32.23	0.86	0.86

Table 170

Expression of each cDNA in undifferentiated NT2 cells, in NT2 cells cultured in the presence of retinoic acid, or in NT2 cells that were cultured in the presence of retinoic acid and then further cultured in the presence of cell-division inhibitor added (This table also contains clones without description in Examples)

In the table, NT2, NT2_RA, and NT2_RA_INHIB represent untreated NT2 cells, retinoic acid-treated NT2 cells, and retinoic acid/inhibitor-treated NT2 cells, respectively. The assay was performed in triplicate (n=3), and each result was shown in the column of exp.1, exp.2, or exp.3. In addition, "t-test N/R" and "t-test N/I" represent results of test for significance of difference between the untreated cells and the retinoic acid-treated cells, and between the untreated cells and the retinoic acid/inhibitor-treated cells, respectively. The results of the test are shown in the columns of *:$p<0.05$ and **:$p<0.01$.

Clone	NT2			NT2 RA			NT2 RA INHIB			ttest N/R	+ −	ttest N/I	+ −
	exp.1	exp.2	exp.3	exp.1	exp. 2	exp.3	exp.1	exp.2	exp.3				
GAPDH(Cr1)	3.53	1.08	0.98	2.92	2.49	2.8	1.76	2.59	1.52				
β actin(Cr2)	155.4	118	99.68	148.5	110.7	101.3	114.7	105.8	151.1				
ADRGL1000005	4.01	2.03	1.55	4.05	3.65	3.6	2.27	2.93	4.24				
ADRGL1000007	11.08	5.73	7.92	15.42	10.6	13.87	8.99	8.17	9.15				
ADRGL1000009	1.11	0.72	1.04	1.66	1.89	1.03	1.22	1.62	1.58			*	+
ADRGL1000011	4.27	2.7	2.85	4.32	4.35	3.38	2.76	3.27	3.06				
ADRGL1000027	1.83	0.38	0.56	0.97	0.62	0.99	0.92	1.33	1.5				
ADRGL1000058	3.65	2.58	1.37	2.92	3.36	2.75	2.25	3.51	2.7				
ADRGL1000069	3.25	1.85	3.28	1.86	2.53	2.85	2.01	2.89	2.7				
ADRGL1000077	13.48	10.41	6.71	19.62	17.92	22.59	11.6	16.66	19.34	*	+		
ADRGL1000092	5.73	2.8	4.51	7.31	5.01	4.83	3.24	6.16	7.22				
ADRGL1000099	5.64	3.42	2.08	5.59	3.73	4.24	3.98	3.98	4.06				
ADRGL1000136	9.97	3.52	4.19	5.77	4.73	5.86	6.61	5.16	5.49				
ADRGL1000147	23.09	13.85	11.7	14.77	14.96	14.89	17.7	13.3	19.47				
ADRGL1000159	6.11	2.22	3.37	5.24	2.88	4.15	2.76	2.93	3.59				
ADRGL1000160	7.16	3.48	4.19	5.94	4.59	3.41	3.95	4.67	4.25				
ADRGL1000171	4.84	2.99	3.23	3.52	4.19	4.37	2.55	3.88	3.45				
ADRGL1000181	5.1	3.65	2.6	3.16	4.06	2.97	2.64	3.06	3.44				
BGGI11000015	13.95	6.83	6.72	9.61	9.19	10.24	9.94	10.66	10.13				
BGGI11000016	15.49	5.92	7.09	11.88	11.38	8.72	11.82	10.98	10.51				
BGGI11000017	7.89	2.99	3.25	4.94	4.94	4.93	3.55	4.27	3.52				
BGGI11000022	8.77	5.14	5.91	7.12	7.05	4.54	5.71	5.59	5.9				
BGGI11000031	4.71	2.16	2.74	4.09	3.29	3.96	4.02	3.67	2.33				
BGGI11000042	6.37	5.24	3.74	5.63	6.22	4.36	4.66	5.2	4.04				
BGGI11000046	19.01	12.57	9.23	12.39	15.7	12.37	8.8	10.92	9.17				
BNGH41000020	859	910.1	603	164	319.2	267.4	638.2	771.6	845.4	**	-		
BNGH41000025	5.35	2.06	2.09	2.76	2.76	3.77	4.23	2.01	3.06				
BNGH41000026	16.2	7.69	7.05	9.34	11.37	9.66	10.13	7.16	10.71				
BNGH41000027	2.31	2.18	2.5	2.9	3.01	2.82	3.68	3.48	4.21	**	+	**	+
BNGH41000035	14.57	8.83	9.36	10.92	9.55	14.75	15.02	15.18	12.2				
BNGH41000037	10.56	7.46	6.2	8.16	9.21	6.42	3.37	5.45	4.98				
BNGH41000042	77.1	50.85	58.45	47.64	53.39	62.67	28.12	35.48	23.44			*	-
BNGH41000048	3.5	2.19	1.91	4.28	2.87	2.4	1.63	3.01	1.78				
BNGH41000056	2.57	2.01	1	1.91	2.63	2.15	1.41	2.4	1.79				
BNGH41000087	9.84	5.84	5.53	12.49	10.24	10.25	11.74	9.68	8.53				
BNGH41000091	3.37	2.59	1.21	3.29	3.01	1.55	2.95	2.57	2.13				
BNGH41000157	10.63	5.64	6.15	8.53	9.05	7.74	6.38	6.68	5.75				
BNGH41000169	3.77	4.34	3.82	4.9	3.48	3.32	3.4	4.16	4.19				
BNGH41000181	2.47	1.59	1.84	2.93	2.1	1.8	1.7	2.66	1.59				
BNGH41000198	8.13	4.64	3.79	5.48	4.35	5.59	4.3	4.15	4.35				
BNGH41000219	9.61	3.92	4.87	4.17	5.29	5.45	5.24	7.12	7.13				
BNGH41000229	19.61	13.28	8.68	10.86	11.27	9.36	7.9	9.5	10.85				
BNGH41000237	10.9	5.47	6.45	6.65	6.97	7.79	6.36	6.25	5.44				
BNGH41000238	4.58	7	3.45	5.91	4.68	4.34	4.33	5.44	4.22				
BNGH41000243	13.85	8.69	8.48	10.19	9.71	8.97	8.23	4.87	5.54				
BNGH41000270	5.83	2.62	2.35	2.3	3.05	3.44	2.59	3.49	1.3				
BRAWH1000004	4.19	2.83	2.48	5.04	3.15	3.26	1.44	3.45	2.05				
BRAWH1000018	4.85	1.95	2.29	7.47	8.8	8.85	8.68	6.61	7.96	**	+	*	+
BRAWH1000021	6.52	5.06	5.87	5.09	6.94	6.44	2.89	6.23	4.28				
BRAWH1000027	11.64	8.86	7.19	8.24	10.39	11.51	5.58	7.13	8.24				
BRAWH1000029	9.58	5.15	3.52	6.01	6.72	6	5.08	5.12	5.84				
BRAWH1000040	4.6	1.89	2.14	2.92	2.71	2.7	2.92	2.5	3.01				
BRAWH1000050	11.48	4.95	5.19	9.74	7.25	8.62	8.25	8.09	8.93				
BRAWH1000051	8.18	3.93	3.19	6.15	5.72	6.02	5.01	4.25	4.44				

Table 349

Y79AA1002361	5.46	3.35	2.57	6.5	7.83	6.14	2.75	4.60	4.6	*	+		
Y79AA1002365	1.93	1.66	1.86	2.93	2.21	2.54	1.34	2.05	2.05	*	+		
Y79AA1002373	3.38	1.43	1.37	3.37	3.29	2.38	2.95	2.21	2.21				
Y79AA1002376	434.81	300.04	466.40	120.28	171.61	120.00	316.81	454.58	454.6	**	-		
Y79AA1002378	5.45	6.92	5.32	7.99	10.13	8.03	4.87	4.92	4.92	*	+		
Y79AA1002381	11.63	11.08	9.56	16.28	16.98	14.53	7.89	7.01	7.01	**	+	**	-
Y79AA1002388	4.34	4.47	7.01	11.41	12.79	9.45	5.70	6.37	6.37	*	+		
Y79AA1002399	4.43	1.48	1.47	4.2	2.82	2.25	3.39	3.35	3.35				
Y79AA1002407	1.81	1.09	1.32	2.36	2.58	2.43	1.55	2.35	2.35	**	+		
Y79AA1002413	15.88	6.76	10.60	19.95	26.46	17.33	9.58	12.56	12.56				
Y79AA1002416	5.12	2.89	2.97	4.45	4.32	5.10	4.13	4.19	4.19				
Y79AA1002429	2.82	1.17	1.77	2.75	1.85	2.91	4.10	5.62	5.62			*	+
Y79AA1002431	4.04	2.82	3.86	2.55	4.38	4.86	4.06	5.56	5.56	-			
Y79AA1002433	11.76	5.78	6.28	9.49	4.53	7.78	4.34	8.17	8.17				
Y79AA1002445	10.95	9.11	9.11	11.15	8.78	14.80	10.37	11.14	11.14				
Y79AA1002461	10.04	5.58	4.92	9.55	8.99	8.05	5.89	7.75	7.75				
Y79AA1002466	22.18	13.94	11.33	23.59	18.02	25.25	10.79	17.76	17.76				
Y79AA1002471	5.76	3.00	5.65	6.94	8.49	9.26	5.31	7.89	7.89	*	+		
Y79AA1002472	12.12	5.83	9.20	16.86	14.60	20.34	6.74	12.38	12.38	*	+		
Y79AA1002474	3.46	0.84	1.92	1.74	1.49	1.64	2.77	1.35	1.35				
Y79AA1002482	13.92	8.55	11.10	23.82	23.90	29.62	10.40	14.99	14.99	**	+		
Y79AA1002487	1.72	0.87	1.11	1.3	1.59	1.75	1.57	1.93	1.93				
Y79AA1002490	13.58	4.80	6.45	5.13	6.72	3.78	4.31	7.19	7.19				
Y79AA1002493	5.77	2.96	3.11	8.04	10.37	7.90	4.77	5.75	5.75	*	+		
ZRV6C1006278	1.43	0.95	1.01	1.16	2.05	0.47	1.35	2.06	2.06				

[0245] The correspondence of the full-length nucleotide sequences of the present invention and the corresponding deduced amino acid sequences with the clone names are shown below.

Table 350

clone name	name of full-length nucleotide sequence	SEQ ID of full-length nucleotide sequence	SEQ ID of deduced amino acid sequence
HEMBA1000005	C-HEMBA1000005	10468	10469
HEMBA1000030	C-HEMBA1000030	10470	
HEMBA1000046	C-HEMBA1000046	10471	
HEMBA1000050	C-HEMBA1000050	10472	
HEMBA1000076	C-HEMBA1000076	10473	10474
HEMBA1000156	C-HEMBA1000156	10475	10476
HEMBA1000158	C-HEMBA1000158	10477	10478
HEMBA1000168	C-HEMBA1000168	10479	10480
HEMBA1000185	C-HEMBA1000185	10481	10482
HEMBA1000193	C-HEMBA1000193	10483	10484
HEMBA1000227	C-HEMBA1000227	10485	10486
HEMBA1000288	C-HEMBA1000288	10487	
HEMBA1000302	C-HEMBA1000302	10488	
HEMBA1000304	C-HEMBA1000304	10489	10490
HEMBA1000307	C-HEMBA1000307	10491	10492
HEMBA1000369	C-HEMBA1000369	10493	10494
HEMBA1000387	C-HEMBA1000387	10495	
HEMBA1000392	C-HEMBA1000392	10496	
HEMBA1000460	C-HEMBA1000460	10497	
HEMBA1000488	C-HEMBA1000488	10498	10499
HEMBA1000491	C-HEMBA1000491	10500	10501
HEMBA1000501	C-HEMBA1000501	10502	
HEMBA1000508	C-HEMBA1000508	10503	
HEMBA1000520	C-HEMBA1000520	10504	
HEMBA1000531	C-HEMBA1000531	10505	10506
HEMBA1000534	C-HEMBA1000534	10507	
HEMBA1000555	C-HEMBA1000555	10508	10509
HEMBA1000568	C-HEMBA1000568	10510	
HEMBA1000588	C-HEMBA1000588	10511	
HEMBA1000608	C-HEMBA1000608	10512	10513

PLACE1004672	C-PLACE1004672	12721	12722
PLACE1004674	C-PLACE1004674	12723	12724
PLACE1004691	C-PLACE1004691	12725	
PLACE1004722	C-PLACE1004722	12726	12727
PLACE1004736	C-PLACE1004736	12728	12729
PLACE1004740	C-PLACE1004740	12730	
PLACE1004743	C-PLACE1004743	12731	12732
PLACE1004751	C-PLACE1004751	12733	12734
PLACE1004777	C-PLACE1004777	12735	12736
PLACE1004804	C-PLACE1004804	12737	12738
PLACE1004814	C-PLACE1004814	12739	12740
PLACE1004824	C-PLACE1004824	12741	12742
PLACE1004868	C-PLACE1004868	12743	12744
PLACE1004885	C-PLACE1004885	12745	12746
PLACE1004902	C-PLACE1004902	12747	12748
PLACE1004918	C-PLACE1004918	12749	12750
PLACE1004930	C-PLACE1004930	12751	12752
PLACE1004934	C-PLACE1004934	12753	
PLACE1004937	C-PLACE1004937	12754	12755
PLACE1004969	C-PLACE1004969	12756	12757
PLACE1004982	C-PLACE1004982	12758	12759
PLACE1005026	C-PLACE1005026	12760	12761
PLACE1005027	C-PLACE1005027	12762	
PLACE1005046	C-PLACE1005046	12763	
PLACE1005077	C-PLACE1005077	12764	
PLACE1005101	C-PLACE1005101	12765	12766
PLACE1005102	C-PLACE1005102	12767	12768
PLACE1005111	C-PLACE1005111	12769	
PLACE1005181	C-PLACE1005181	12770	
PLACE1005187	C-PLACE1005187	12771	12772
PLACE1005206	C-PLACE1005206	12773	12774
PLACE1005232	C-PLACE1005232	12775	
PLACE1005243	C-PLACE1005243	12776	12777
PLACE1005261	C-PLACE1005261	12778	12779
PLACE1005266	C-PLACE1005266	12780	
PLACE1005277	C-PLACE1005277	12781	12782
PLACE1005287	C-PLACE1005287	12783	12784
PLACE1005305	C-PLACE1005305	12785	12786
PLACE1005308	C-PLACE1005308	12787	12788

Table 352

Expression of each cDNA in synovial cells or in the synovial cells in the presence of TNF (This table also contains clones without description in Examples)

In the table, Synoviocyte and Synoviocyte_TNF represent synovial cells and TNF-treated synovial cells, respectively. The assay was performed in triplicate (n=3), and each result is shown in the column of exp.1, exp.2, or exp.3. In addition, "t-test vs TNF" represents a result of test for significance of difference between the untreated synovial cells and the TNF-treated synovial cells. The increase and decrease in the expression level of a particular gene in response to TNF are represented by + and -, respectively. The results of test for significance of difference are shown in the columns of *:$p<0.05$ and **:$p<0.01$.

Clone	Synoviocyte			Synoviocute_TNF			t test vs TNF	INC. and DEC.
	exp. 1	exp. 2	exp. 3	exp. 1	exp. 2	exp. 3		

PLACE1005193	1.48	3.78	1.71	3.84	2.91	2.61	
PLACE1005200	1.35	4.68	2.61	2.47	3.75	3.1	
PLACE1005206	2.43	6.48	4.26	3.35	3.95	2.95	
PLACE1005216	1.53	5.46	4.44	5.6	6.51	4.12	
PLACE1005223	1.43	6.21	5	4.38	5.66	3.27	
PLACE1005225	1.36	3.01	3.49	3.33	3.32	4.65	
PLACE1005232	1.86	3.31	4.87	5.63	6.19	3.88	
PLACE1005239	1.06	4.3	2.32	2.84	2.86	2.41	
PLACE1005243	4.35	7.32	5.41	8.48	7.49	10.75	
PLACE1005250	4.24	10.31	7.98	4.38	5.9	8.88	
PLACE1005261	3.21	7.43	4.74	4.78	5.82	3.51	
PLACE1005266	1.05	4.47	2.82	2.28	4.43	2.76	
PLACE1005271	4.66	5.31	8.79	5.87	11.16	7.95	
PLACE1005277	2.06	3.48	2.35	2.62	1.98	2.64	
PLACE1005287	3.63	4.31	5.87	2.98	5.06	6.91	
PLACE1005299	24.16	22.75	48.29	35.17	24.24	41.06	
PLACE1005305	6.81	8.46	11.13	10.67	11.85	16.25	
PLACE1005307	1.59	5.44	4.14	3.15	5.42	4.84	
PLACE1005308	2.41	4.96	3.95	5.32	5.99	5.79	
PLACE1005313	1.08	3.83	1.6	1.8	2.05	1.8	
PLACE1005320	1.36	3.65	3.34	3.39	4.05	2.26	
PLACE1005327	10.78	8.74	16.8	10.36	7.95	4.43	
PLACE1005331	2.28	4.92	5.28	4.66	4.97	3.33	
PLACE1005335	1.53	3.8	2.24	2.03	3.22	2.42	
PLACE1005336	9.12	12.58	16.58	16.39	16.99	20.15	
PLACE1005351	2.62	8.18	10.17	9.28	8.66	9.52	
PLACE1005366	2.04	6.93	3	2.99	3.71	4.23	
PLACE1005373	1.77	6.34	4.44	3.91	5.36	3.37	
PLACE1005374	3.29	9.47	11.4	7.35	10.22	12.41	
PLACE1005383	8.16	7.54	12.81	7.21	5.93	4.03	
PLACE1005388	0.33	2.04	1.56	1.92	3.67	2.2	
PLACE1005409	2.97	5.02	4.99	3.9	4.23	2.97	
PLACE1005410	12.41	16.44	18.89	24.38	20.98	27.1	* +
PLACE1005426	5.16	7.48	9.06	5.51	7.67	5.45	
PLACE1005431	12.6	15.65	22.53	19.64	26.25	23.75	
PLACE1005453	1.4	10.38	3.93	4.85	4.45	3.28	
PLACE1005467	3.09	11.87	7	5.57	11.63	7.28	
PLACE1005471	1.6	1.94	1.66	2.29	1.52	1.28	
PLACE1005476	0.42	1.73	1.24	1.6	1.57	1.46	

Table 353

Expression of each cDNA in skin-derived fibroblast cells exposed and unexposed to ultraviolet light (the table also includes clones that are not described in Examples)

In the table, UV_0h represents skin-derived fibroblast cells without ultraviolet irradiation; UV_4h and UV_24h represent skin-derived fibroblast cells 4 and 24 hours, respectively, after the irradiation. The assay was performed in triplicate (n=3) and each result is shown in the column of Exp1, Exp2, or Exp3. "t-test 0/4" and "t-test 0/24" represent the results of the test for significant difference between the unexposed cells and the cells 4 hours after the irradiation, and between the unexposed cells and the cells 24 hours after the irradiation, respectively. The table also includes the information on an increase (+) or decrease (-) in the expression level of the gene in the exposed cells 4 hours or 24 hours after the ultraviolet light irradiation. The results of the test for significant difference are shown in the columns of *p<0.05 and **p<0.01.

Clone	UV 0h			UV 4h			UV 24h			t test		4h 24h	
	Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	Exp. 1	Exp. 2	Exp. 3	0/4	0/24	+/-	+/-
GAPDH(Cr1)	0	1.29	0.1	0.9	0.06	1.18	1.49	0.47	0				
β actin(Cr2)	256.82	283.53	414.29	388.38	117.29	329.8	189.18	190.26	157.87		*		-
ADRGL1000005	15.9	10.68	19.67	3.3	6.44	12.69	6	3.06	5		*		-
ADRGL1000007	47.47	31.62	85.7	41.54	41.35	40.62	31.64	14.77	31.5				
ADRGL1000009	3.97	2.45	8.72	6.06	2.65	3.32	3.72	1.8	2.91				
ADRGL1000011	21.55	13.26	21.8	18.36	12.63	13.95	15.62	6.5	14.45				
ADRGL1000027	2.4	1.68	5.6	4.02	2.48	2.04	3.18	0.81	3.55				
ADRGL1000058	84.24	29.04	76.55	95.27	68.98	72.58	39.84	22.31	39.98				
ADRGL1000069	7.61	6.31	10.67	3.58	5.86	4.59	2.92	1.14	2.62		*		-
ADRGL1000077	4.08	5.99	6.34	5.76	3.87	4.68	4.23	2	3.08				
ADRGL1000092	41.45	38.57	55.77	73.06	40.91	54.59	24.67	18.9	27.36		*		-
ADRGL1000099	43.57	33.01	48.6	56.04	29.24	45.47	24.87	18.08	20.27		*		-
ADRGL1000136	52.22	43.6	70.27	58.84	40.95	44.91	35.09	21.07	29.76		*		-
ADRGL1000147	6.66	6.78	11.64	6.52	5.38	7	5.38	2.59	5.89				
ADRGL1000159	7.28	7.31	7.55	10.23	10.38	9.89	7.3	4.68	8.62	**		+	
ADRGL1000160	11.62	12.89	8.28	9.39	13.77	23.6	7.39	5.18	9.59				
ADRGL1000171	4.47	4.72	5.01	4.83	6.43	4.19	3.69	1.77	4.29				
ADRGL1000181	9.73	12.6	18.02	18.65	11.48	13.93	9.96	11.18	7.77				
BGGI11000015	25.13	21.03	22.91	10.68	12.73	20.09	10.32	15.5	18.5		*		-
BGGI11000016	63.98	55.25	74.82	18.05	36.94	8.26	17.67	40.65	37.24	*	*	-	-
BGGI11000017	8.13	6.51	11.46	3.65	5.27	5.54	2.72	4.69	3.8		*		-
BGGI11000022	12.98	14.45	15.11	7.84	9.62	8.77	7.97	8.92	10.08	**	**	-	-
BGGI11000031	13.67	9.32	14.45	9.12	13.53	12.58	6.75	10.28	15.5				
BGGI11000042	78.81	92.28	77.71	51.19	53.47	19.5	23.41	16.53	22.63	*	**	-	-
BGGI11000046	59.14	59.17	43.06	30.88	42.51	35.11	16	15.29	7.23		**		-
BNGH41000025	34.23	58.36	71.87	11.96	22.6	19.45	12.51	15.56	19.08	*	*	-	-
BNGH41000026	8.61	10.35	11.92	5.79	4.65	4.41	2.7	3.65	4.11	**	**	-	-
BNGH41000027	36.04	26.15	57.91	21.21	34.28	46.33	28.86	28.53	19.37				
BNGH41000035	71.93	95.4	103.3	77.48	91.38	82.2	85.4	91.4	89.21				
BNGH41000037	11.37	8.43	18.43	4.88	12.04	10.79	4.26	3.88	5.78				
BNGH41000042	153.34	222.69	94.88	128.41	120.85	102.56	66.52	26.75	52.39		*		-
BNGH41000048	115.13	80.94	131.08	158.03	99.22	95.02	70.52	58.67	62.66		*		-
BNGH41000056	6.81	7.33	32.46	17.81	11.49	11.22	6.84	4.36	6.34				
BNGH41000087	7.57	4.78	6.77	6.26	6.74	6.12	2.23	3.11	5.45				
BNGH41000091	5.88	4.66	7.21	3.92	3.81	2.29	2.51	1.95	5.23	*		-	
BNGH41000157	24.78	9.57	39.68	15.95	28.36	14.05	14.96	12.43	25.4				
BNGH41000169	4.77	2.7	8.76	3.03	4.07	2.47	2.48	1.85	2.4				
BNGH41000181	15.03	14.16	15.82	9.14	8.43	9.02	9.57	5.48	4.7	**	**	-	-
BNGH41000198	5.23	7.17	13.44	2.81	5.92	4	2.64	2.63	2.78				
BNGH41000219	55.36	63.96	42.98	30.63	34.86	27.19	11.04	4.75	5.11	*	**	-	-
BNGH41000229	41.48	41.07	32.45	12.86	20.86	15.06	12.11	29.5	42.2	**		-	
BNGH41000237	30.57	28.92	29.88	23.95	17.14	16.36	7.62	11.39	18.2	*	**	-	-
BNGH41000238	12.97	6.92	11.13	3.1	5.96	5.05	3.21	2.99	4.83	*	*	-	-
BNGH41000243	37.29	22.23	38.12	21.69	20.76	22.29	17.48	13.04	12		*		-
BNGH41000270	7.24	2.74	13.66	5.03	4.81	3.91	2.55	1.06	3.15				
BRAWH1000004	26.05	12.1	22.36	14.77	13.7	15.56	10.21	9.28	9.3				
BRAWH1000018	16.02	18.04	23.1	10.35	11.87	13.62	8.4	6.81	8.26	*	**	-	-
BRAWH1000021	13.77	12.07	18.61	14.58	14.48	10.65	13.45	8.59	11.48				
BRAWH1000027	4.8	4.82	5.71	4.63	4.59	5.52	2.19	2.04	7.42				
BRAWH1000029	7.2	4.85	5.05	4.67	2.83	2.65	2.93	2.18	1.97		*		-
BRAWH1000040	20.85	33.58	27.15	16.04	13.44	12.14	8.98	5.99	6.77	*	**	-	-
BRAWH1000050	86.78	63.26	107.91	121.47	88.32	92.39	77.36	45.55	64.9				
BRAWH1000051	3.25	3.15	8.62	2.34	1.27	1.81	2.29	1.14	1.52				
BRAWH1000060	103.56	87.24	102.14	122.05	99.97	107.12	58.34	59.07	66.98		**		-
BRAWH1000075	6.97	6.63	15	3.29	4.01	3.69	3.52	2.95	3.34				
BRAWH1000081	23.41	12.71	28.79	20.72	20.86	22.65	19.13	9.85	15.04				
BRAWH1000084	219.94	140.27	3.27	8.21	5.55	1.75	106.89	121.2	155.45				
BRAWH1000095	6.67	5.04	6.84	7.47	5.22	4.62	3.81	0.91	1.79		*		-

Table 478

PLACE1005101	11.5	9.29	11.94	9.18	4.8	5.47	5.22	3.69	6.78	*	**	- -
PLACE1005102	22.17	25.98	27.54	6.07	7.69	6.94	7.15	5.65	7.82	**	**	- -
PLACE1005108	10.15	7.73	6.02	2.99	6.05	3.33	4.8	7.23	6.47			
PLACE1005110	3.97	2.39	3.45	3.59	3.78	1.51	2.14	1.33	2.15			
PLACE1005111	23.94	21.69	16.98	14.04	21.5	8.57	20.32	16.74	23.71			
PLACE1005123	16.94	14.46	12.96	5.45	9.5	5	6.89	4.29	5.82	*	**	- -
PLACE1005124	9.14	6.62	6.15	2.06	5.47	1.8	6.61	3.46	5.33	*		-
PLACE1005128	6.83	4.81	4.87	1.09	3.42	1.91	3.3	3.63	2.82	*	*	- -
PLACE1005130	12.43	17.68	12.68	4.58	11.05	5.79	12.55	5.44	10.87			
PLACE1005141	6.07	3.99	5.18	6.23	2.88	1.1	9.65	2.17	2.82			
PLACE1005146	10.52	9.7	6.88	6.24	10.69	5.88	5.25	8.14	5.49			
PLACE1005152	91.15	76.64	75.79	51.06	95.95	52.59	42.4	38.1	38.75		**	-
PLACE1005157	5.11	3.75	6.06	2.82	4.86	2.4	1.9	2.79	1.7		*	-
PLACE1005162	24.79	23.25	27.03	17.82	26.77	20.32	10.52	15.51	11.65		**	-
PLACE1005170	9.55	7.54	6.99	11.08	19.85	14.4	3.82	8.2	5.94			
PLACE1005176	5.55	5.17	6.85	2.52	4.13	3.01	2.09	2.54	1.26	*	**	- -
PLACE1005181	10.56	18.07	15.09	7.46	9.06	8.01	10.91	12.85	10.11	*		-
PLACE1005184	3.64	4.4	5.5	5.28	11.77	4.26	3.84	3.69	3.06			
PLACE1005186	5.96	5.07	5.66	2.88	2.54	3.26	3.64	4.33	4.72	**	*	- -
PLACE1005187	20.53	14.71	18.55	8.5	10.66	10.36	12.23	12.87	7.61	*	*	- -
PLACE1005189	8.28	7.72	11.92	4.24	7.19	3.99	6.84	7.52	5.99			
PLACE1005193	39.26	44.11	39.59	31.34	38.66	28.91	36.03	40.56	33.69			
PLACE1005200	1391.4	1317.2	1202.3	1770.3	2457.3	1744.3	1189.8	1397.9	586.38	*		+
PLACE1005206	48.27	41.57	88.17	48.38	52.86	50.82	27.19	13.53	58.32			
PLACE1005216	10.1	9.74	10.26	5.79	10.41	5.95	3.4	3.26	4.05		**	-
PLACE1005223	36.86	44.94	37.06	23.02	26.39	16.59	23.41	26.05	19.76	*	**	- -
PLACE1005225	5.34	5.81	6.83	4.25	3.02	5.27	2.59	3.79	3.7		*	-
PLACE1005232	37.45	31.95	45.29	20.08	17.68	11.81	24.42	25.92	23.95	**	*	- -
PLACE1005239	7.93	6.66	12.45	5.29	3.66	4.36	3.81	3.89	4.86			
PLACE1005243	16.13	27.58	27.13	19.28	15.8	19.25	6.8	13.48	9.67		*	-
PLACE1005250	5.37	6.75	7.77	5.96	4.93	3.55	3.78	5.49	3.24			
PLACE1005261	61.12	61.95	56.67	47.53	36.14	42.92	20.88	23.52	21.14	**	**	- -
PLACE1005266	7.03	6.91	9.71	5.82	8.14	5.96	4.18	3.69	5.53		*	-
PLACE1005271	8.47	8.61	6.86	4.77	7.74	3.27	3.65	3.57	3.35		**	-
PLACE1005277	20.92	15.1	22.31	9.09	13.8	9.19	14.68	15.64	18.36	*		-
PLACE1005287	15.1	8.12	14.31	5.25	6.44	6.19	5.01	4.78	3.02	*	*	- -
PLACE1005299	10.04	6.09	8.79	4.5	5.75	7.77	4.03	4.98	7.58			
PLACE1005305	8.97	7.38	9.77	4.47	3.45	4.18	3.14	3.99	3.81	**	**	- -
PLACE1005307	12.01	9.78	33.93	6.5	6.01	6.92	5.78	5.91	8.37			
PLACE1005308	6.72	9.28	13.18	4.37	5.39	4.05	5.69	4.54	7.02			
PLACE1005313	8.46	6.04	10.79	5.16	6.95	3.74	4.51	3	4		*	-
PLACE1005320	9.29	12.54	14.31	7.32	9.29	5.14	4.92	4.65	5.56		**	-
PLACE1005327	31	25.4	35.29	16.09	17.4	11.88	9.82	14.36	14.83	**	**	- -
PLACE1005331	13.95	13.36	13.69	9.09	7.58	7.27	7.77	10.5	7.36	**	**	- -
PLACE1005335	11.38	7.64	13.28	5.94	7.87	3.65	8.18	25.07	9.78			
PLACE1005336	29.59	23.98	23.59	14.99	18	12.79	23.63	28.14	27.34	*		-
PLACE1005351	11.96	8.58	19.03	4.6	4.51	3.68	3.27	6.24	4.61	*		-
PLACE1005366	73.8	70.81	70.61	45.9	65.72	42.52	55.33	53.05	50.72	*	**	- -
PLACE1005373	9.8	6.9	15.51	3.87	3.73	2.69	2.9	3.58	2.99	*	*	- -
PLACE1005374	31.25	37.89	30.27	12.29	20.74	12.12	33.17	26.39	29.29	**		-
PLACE1005383	9.15	7.91	6.27	5.38	5.79	4.82	3.77	5.77	7.02	*		-
PLACE1005388	14.78	7.34	14.13	9.31	7.11	6.02	6.28	5.49	5.89			
PLACE1005409	11.86	10.31	14.09	4.95	5.84	5.2	5.09	4.29	5.35	**	**	- -
PLACE1005410	13.35	9.74	14.55	5.14	6.18	4.53	6.86	5.79	5.13	**	*	- -
PLACE1005426	10.65	4.8	11.31	4.23	3.51	3	2.46	6.49	1.78			
PLACE1005431	8.27	7.3	10.2	3.04	3.82	2.32	3.59	3.79	5.31	**	*	- -
PLACE1005453	7.65	9.23	18.96	3.09	5.38	3.63	2.3	4.42	3.43			
PLACE1005467	10.75	11.01	23.28	4.33	7.93	7.46	6.29	7.36	5.29			
PLACE1005471	7.1	9.43	5.6	3.8	6.04	3.15	3.31	6.18	12.95			
PLACE1005476	29.52	27.39	29.6	15.57	12.74	15.37	14.04	14.17	16.62	**	**	- -
PLACE1005477	9.37	7.91	13.74	3.68	6.31	4.63	5	3.74	6.24	*	*	- -
PLACE1005480	7.1	8	8.36	5.61	4.81	4.45	4.92	2.94	2.27	**	**	- -
PLACE1005481	10.21	6.44	10.18	3.66	4.76	4.41	5.76	4.63	3.43	*	*	- -
PLACE1005494	9.19	9.94	10.69	3.34	4.05	3.41	4.87	3.69	4.02	**	**	- -

Y79AA1000342//Zinc finger, C2H2 type
Y79AA1000349//Double-stranded RNA binding motif
Y79AA1000627//Zinc finger, C2H2 type
Y79AA1000705//Helicases conserved C-terminal domain
Y79AA1000752//KH domain family of RNA binding proteins
Y79AA1000833//Tubulin
Y79AA1001048//Acyl-CoA dehydrogenases
Y79AA1001391//Homeobox domain
Y79AA1001394//ATPases associated with various cellular activities (AAA)
Y79AA1001493//Ubiquitin-conjugating enzymes
Y79AA1001613//Zinc finger, C2H2 type
Y79AA1001874//TNFR/NGFR cysteine-rich region
Y79AA1002027//Ubiquitin-conjugating enzymes
Y79AA1002139//DnaJ, prokaryotic heat shock protein
Y79AA1002208//Ank repeat
Y79AA1002246//C2 domain
Y79AA1002307//Fibronectin type III domain
Y79AA1002472//Zinc finger, C2H2 type
HEMBA1003538//CUB domain HEMBA1003645//WD domain, G-beta repeats //Src homology domain 3 HEMBA1005206//Glutathione S-transferases.
HEMBA1006521//Alcohol/other dehydrogenases, short chain type
HEMBB1001482//Zinc finger, C2H2 type HEMBB1001915//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 HEMBB1002044//Cadherin MAMMA1000183//Zinc finger, C2H2 type MAMMA1000897//von Willebrand factor type A domain MAMMA1001080//IG superfamily MAMMA1002498//IG superfamily MAMMA1002573//KH domain family of RNA binding proteins MAMMA1002617//Zinc finger, C2H2 type
NT2RM1000833//eubacterial secY protein NT2RM2001797//Zinc finger, C2H2 type
NT2RP1001013//Zinc finger, C2H2 type NT2RP2001233//Zinc finger, C2H2 type
NT2RP2001440//14-3-3 proteins NT2RP2002105//7 transmembrane receptor (rhodopsin family) NT2RP3001723//Laminin G domain NT2RP3001938//Eukaryotic protein kinase domain NT2RP3002330//Elongation factor Tu family (contains ATP/GTP binding P-loop) NT2RP3003133//Zinc finger, C2H2 type
NT2RP3003500//Eukaryotic protein kinase domain NT2RP3003799//C2 domain
NT2RP3003800//Eukaryotic protein kinase domain NT2RP3004013//Double-stranded RNA binding motif NT2RP3004125//Zinc finger, C2H2 type
OVARC1001244//Bromodomain OVARC1001496//D-isomer specific 2-hydroxyacid dehydrogenases
PLACE1000007//Ubiquitin carboxyl-terminal hydrolases family 2 //Ubiquitin carboxyl-terminal hydrolases family 2 PLACE1001118//Zinc finger, C2H2 type PLACE1010310//Zinc finger, C2H2 type PLACE1011896//wnt family of developmental signaling proteins PLACE3000124//Src homology domain 2
PLACE4000100//D-isomer specific 2-hydroxyacid dehydrogenases
PLACE4000259//Helicases conserved C-terminal domain PLACE4000261//Bromodomain SKNMC1000013//ABC transporters SKNMC1000091//Basic region plus leucine zipper transcription factors THYRO1000343//Src homology domain 3 THYRO1000569//Zinc finger, C2H2 type THYRO1001189//Zinc finger, C2H2 type Y79AA1002103//Zinc finger, C2H2 type PLACE3000350//Eukaryotic protein kinase domain
PLACE4000156//Zinc finger, C2H2 type

EXAMPLE 18

Classification of cDNA clones into functional categories based on the full-length nucleotide sequences

[0257] Prediction of functions of proteins encoded by the clones and the categorization thereof were performed based on the results of homology search (see Homology search results 6, 12, 13 and 14) of the databases, GenBank, SwissProt and UniGene, for the full-length nucleotide sequences of 4997 clones and based on the results of domain search (see Example 17) of the deduced amino acid sequences encoded by the full-length nucleotide sequences. The target 4997 clones are listed below:

HEMBA1000005, HEMBA1000012, HEMBA1000020, HEMBA1000030, HEMBA1000042, HEMBA1000046, HEMBA1000050, HEMBA1000076, HEMBA1000129, HEMBA1000141, HEMBA1000150, HEMBA1000156, HEMBA1000158, HEMBA1000168, HEMBA1000185, HEMBA1000193, HEMBA1000201, HEMBA1000213, HEMBA1000216, HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251, HEMBA1000264, HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302,

PLACE1002625, PLACE1002655, PLACE1002665, PLACE1002685, PLACE1002714, PLACE1002722,
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PLACE1002941, PLACE1002962, PLACE1002968, PLACE1002991, PLACE1002993, PLACE1002996,
PLACE1003025, PLACE1003027, PLACE1003030, PLACE1003044, PLACE1003045, PLACE1003092,
PLACE1003100, PLACE1003108, PLACE1003145, PLACE1003174, PLACE1003176, PLACE1003190,
PLACE1003200, PLACE1003205, PLACE1003238, PLACE1003249, PLACE1003256, PLACE1003258,
PLACE1003296, PLACE1003302, PLACE1003334, PLACE1003342, PLACE1003343, PLACE1003353,
PLACE1003361, PLACE1003366, PLACE1003369, PLACE1003373, PLACE1003375, PLACE1003383,
PLACE1003394, PLACE1003420, PLACE1003454, PLACE1003478, PLACE1003493, PLACE1003516,
PLACE1003519, PLACE1003521, PLACE1003528, PLACE1003537, PLACE1003553, PLACE1003566,
PLACE1003584, PLACE1003592, PLACE1003593, PLACE1003596, PLACE1003602, PLACE1003605,
PLACE1003611, PLACE1003618, PLACE1003625, PLACE1003638, PLACE1003669, PLACE1003704,
PLACE1003709, PLACE1003711, PLACE1003723, PLACE1003738, PLACE1003760, PLACE1003762,
PLACE1003768, PLACE1003771, PLACE1003784, PLACE1003795, PLACE1003864, PLACE1003870,
PLACE1003885, PLACE1003886, PLACE1003888, PLACE1003892, PLACE1003900, PLACE1003903,
PLACE1003915, PLACE1003923, PLACE1003936, PLACE1003968, PLACE1004104, PLACE1004114,
PLACE1004118, PLACE1004128, PLACE1004149, PLACE1004156, PLACE1004161, PLACE1004183,
PLACE1004197, PLACE1004203, PLACE1004256, PLACE1004258, PLACE1004270, PLACE1004274,
PLACE1004277, PLACE1004284, PLACE1004289, PLACE1004302, PLACE1004316, PLACE1004336,
PLACE1004358, PLACE1004376, PLACE1004384, PLACE1004388, PLACE1004405, PLACE1004425,
PLACE1004428, PLACE1004437, PLACE1004451, PLACE1004460, PLACE1004471, PLACE1004473,
PLACE1004491, PLACE1004506, PLACE1004510, PLACE1004516, PLACE1004518, PLACE1004548,
PLACE1004550, PLACE1004564, PLACE1004629, PLACE1004645, PLACE1004646, PLACE1004664,
PLACE1004672, PLACE1004674, PLACE1004681, PLACE1004686, PLACE1004691, PLACE1004693,
PLACE1004716, PLACE1004722, PLACE1004736, PLACE1004740, PLACE1004743, PLACE1004751,
PLACE1004777, PLACE1004793, PLACE1004804, PLACE1004814, PLACE1004815, PLACE1004824,
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PLACE1004902, PLACE1004913, PLACE1004918, PLACE1004930, PLACE1004934, PLACE1004937,
PLACE1004969, PLACE1004979, PLACE1004982, PLACE1004985, PLACE1005026, PLACE1005027,
PLACE1005046, PLACE1005052, PLACE1005055, PLACE1005077, PLACE1005085, PLACE1005086,
PLACE1005101, PLACE1005102, PLACE1005108, PLACE1005111, PLACE1005128, PLACE1005146,
PLACE1005162, PLACE1005176, PLACE1005181, PLACE1005187, PLACE1005206, PLACE1005232,
PLACE1005243, PLACE1005261, PLACE1005266, PLACE1005277, PLACE1005287, PLACE1005305,
PLACE1005308, PLACE1005313, PLACE1005327, PLACE1005331, PLACE1005335, PLACE1005373,
PLACE1005374, PLACE1005409, PLACE1005453, PLACE1005467, PLACE1005477, PLACE1005480,
PLACE1005481, PLACE1005494, PLACE1005530, PLACE1005549, PLACE1005550, PLACE1005554,
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PLACE1005804, PLACE1005813, PLACE1005828, PLACE1005850, PLACE1005851, PLACE1005876,
PLACE1005884, PLACE1005890, PLACE1005898, PLACE1005921, PLACE1005923, PLACE1005925,
PLACE1005932, PLACE1005934, PLACE1005936, PLACE1005951, PLACE1005953, PLACE1005955,
PLACE1005966, PLACE1005968, PLACE1005990, PLACE1006002, PLACE1006003, PLACE1006011,
PLACE1006017, PLACE1006037, PLACE1006040, PLACE1006076, PLACE1006119, PLACE1006129,
PLACE1006139, PLACE1006143, PLACE1006157, PLACE1006159, PLACE1006167, PLACE1006170,
PLACE1006195, PLACE1006196, PLACE1006225, PLACE1006236, PLACE1006239, PLACE1006246,
PLACE1006248, PLACE1006288, PLACE1006318, PLACE1006325, PLACE1006335, PLACE1006357,
PLACE1006360, PLACE1006368, PLACE1006371, PLACE1006382, PLACE1006385, PLACE1006412,
PLACE1006414, PLACE1006438, PLACE1006445, PLACE1006469, PLACE1006470, PLACE1006482,
PLACE1006488, PLACE1006492, PLACE1006506, PLACE1006521, PLACE1006531, PLACE1006534,
PLACE1006552, PLACE1006598, PLACE1006615, PLACE1006617, PLACE1006626, PLACE1006640,
PLACE1006673, PLACE1006678, PLACE1006704, PLACE1006731, PLACE1006754, PLACE1006760,
PLACE1006779, PLACE1006782, PLACE1006792, PLACE1006795, PLACE1006805, PLACE1006815,
PLACE1006819, PLACE1006829, PLACE1006867, PLACE1006878, PLACE1006883, PLACE1006901,
PLACE1006917, PLACE1006932, PLACE1006935, PLACE1006956, PLACE1006958, PLACE1006961,
PLACE1006962, PLACE1006966, PLACE1007014, PLACE1007021, PLACE1007045, PLACE1007053,
PLACE1007068, PLACE1007097, PLACE1007105, PLACE1007111, PLACE1007112, PLACE1007140,

Y79AA1001323//Mus musculus mRNA for GSG1, complete cds.
Y79AA1001402//Homo sapiens paraneoplastic cancer-testis-brain antigen (MA4) mRNA, partial cds.
Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.
Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds. Y79AA1002083//H. sapiens mRNA for MUF1 protein.
Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.
Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.
Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.

[0292] Among the clones other than the above-mentioned, there were 36 clones that were similarly classified into the functional categories based on the results of functional domain search using the Pfam program. These clones were categorized as follows.

[0293] Clones presumably belonging to the category of secretory or membrane proteins are two clones, MAMMA1002498 and NT2RM4002287; a clone presumably belonging to the category of glycoproteins-associated proteins is a clone MAMMA1002498; clones presumably belonging to the category of signal transduction-associated proteins are 11 clones, HEMBA1001247, NT2RM2001813, NT2RM4001454, NT2RP2005140, NT2RP2005293, NT2RP3000487, NT2RP3003311, PLACE1000972, PLACE1003723, PLACE1005327, and PLACE3000124; clones presumably belonging to the category of transcription-associated proteins are 12 clones, HEMBA1003257, NT2RM2000101, NT2RM2001797, NT2RP1000101, NT2RP2002208, NT2RP3001214, NT2RP3003278, NT2RP4001235, PLACE1000050, PLACE1001716, PLACE1002499, and PLACE1007544; clones presumably belonging to the category of enzymes and/or metabolism-associated proteins are 2 clones, HEMBA1005732 and MAMMA1000402; clones presumably belonging to the category of DNA- and/or RNA-binding proteins are 4 clones, HEMBA1004596, OVARC1000148, PLACE1003334, and THYRO1001661; a clone presumably belonging to the category of protein synthesis- and/or protein transport-associated proteins is a clone, HEMBA1006284.

[0294] So far, useful information for presuming the functions is unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

[0295] So far, useful information for presuming the functions are unavailable for the remaining 2511 clones. Their functions will possibly be revealed by further analyses. Names of the clones are listed below.

HEMBA1000042, HEMBA1000046, HEMBA1000050, HEMBA1000076, HEMBA1000193, HEMBA1000213,
HEMBA1000227, HEMBA1000231, HEMBA1000243, HEMBA1000244, HEMBA1000251, HEMBA1000264,
HEMBA1000280, HEMBA1000282, HEMBA1000288, HEMBA1000290, HEMBA1000302, HEMBA1000327,
HEMBA1000338, HEMBA1000351, HEMBA1000357, HEMBA1000376, HEMBA1000387, HEMBA1000392,
HEMBA1000396, HEMBA1000428, HEMBA1000442, HEMBA1000456, HEMBA1000459, HEMBA1000460,
HEMBA1000469, HEMBA1000497, HEMBA1000501, HEMBA1000504, HEMBA1000505, HEMBA1000508,
HEMBA1000519, HEMBA1000520, HEMBA1000534, HEMBA1000545, HEMBA1000557, HEMBA1000568,
HEMBA1000575, HEMBA1000594, HEMBA1000604, HEMBA1000622, HEMBA1000636, HEMBA1000655,
HEMBA1000673, HEMBA1000682, HEMBA1000686, HEMBA1000702, HEMBA1000722, HEMBA1000726,
HEMBA1000727, HEMBA1000749, HEMBA1000752, HEMBA1000769, HEMBA1000773, HEMBA1000774,
HEMBA1000843, HEMBA1000867, HEMBA1000869, HEMBA1000872, HEMBA1000876, HEMBA1000908,
HEMBA1000918, HEMBA1000934, HEMBA1000942, HEMBA1000943, HEMBA1000946, HEMBA1000960,
HEMBA1000968, HEMBA1000971, HEMBA1000972, HEMBA1000975, HEMBA1000985, HEMBA1000986,
HEMBA1001008, HEMBA1001009, HEMBA1001020, HEMBA1001022, HEMBA1001024, HEMBA1001026,
HEMBA1001051, HEMBA1001060, HEMBA1001080, HEMBA1001094, HEMBA1001099, HEMBA1001109,
HEMBA1001121, HEMBA1001122, HEMBA1001123, HEMBA1001133, HEMBA1001140, HEMBA1001208,
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HEMBA1001310, HEMBA1001319, HEMBA1001323, HEMBA1001326, HEMBA1001327, HEMBA1001330,
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HEMBA1001939, HEMBA1001940, HEMBA1001942, HEMBA1001950, HEMBA1001964, HEMBA1001987,
HEMBA1002018, HEMBA1002022, HEMBA1002039, HEMBA1002049, HEMBA1002084, HEMBA1002100,
HEMBA1002113, HEMBA1002119, HEMBA1002160, HEMBA1002162, HEMBA1002185, HEMBA1002189,
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PLACE1007178, PLACE1007218, PLACE1007238, PLACE1007242, PLACE1007301, PLACE1007342,
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Homology Search Result Data 1.

[0296] The result of the homology search of the SwissProt using the 5'-end sequence.

[0297] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the organism and the Accession No. of the top hit data, as in the order separated by //.

[0298] Data are not shown for the clones in which the P-value was higher than 1.

[0299] The P-value is a score obtained statistically by taking into account the possible similarity between two sequences. In general, the smaller P-value reflects the higher similarity. (Altschul, S.F., Gish, W., Miller, W., Myers, E.W. & Lipman, D.J. (1990) "Basic local alignment search tool." J. Mol. Biol. 215:403-410; Gish, W. &

States, D.J. (1993) "Identification of protein coding regions by database similarity search." Nature Genet. 3:266-272).

F-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.8e-85:244:75//MUS MUSCULUS (MOUSE).//Q61712
F-HEMBA1000012//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINETRNA LIGASE) (LEURS).//7.6e-57:231:53//CAENORHABDITIS ELEGANS.//Q09996
F-HEMBA1000020//TUBULIN BETA CHAIN.//1.0e-92:143:80//AJELLOMYCES CAPSULATA (HISTOPLASMA CAPSULATUM).//P41742
F-HEMBA1000030//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.021:136:33//PLASMODIUM KNOWLESI (STRAIN NURI).//P04922
F-HEMBA1000042//METALLOTHIONEIN 10-II (MT-10-II).//0.71:64:32//MYTILUS EDULIS (BLUE MUSSEL).//P80247
F-HEMBA1000046//PROTEIN Q300.//0.92:40:37//MUS MUSCULUS (MOUSE).//Q02722
F-HEMBA1000050//COMPETENCE PROTEIN S.//0.50:28:35//BACILLUS SUBTILIS.//P80355
F-HEMBA1000076//ATP SYNTHASE E CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.86:41:41//HOMO SAPIENS (HUMAN).//P56385
F-HEMBA1000111
F-HEMBA1000129//UVSW PROTEIN (DAR PROTEIN).//0.023:68:33//BACTERIOPHAGE T4.//P20703
F-HEMBA1000141//YSY6 PROTEIN.//0.90:29:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38374
F-HEMBA1000150//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//8.4e-16:47:70//HOMO SAPIENS (HUMAN).//P39193
F-HEMBA1000156//IMMEDIATE-EARLY PROTEIN.//8.1e-07:143:28//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042
F-HEMBA1000158//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//7.9e-11:129:40//HOMO SAPIENS (HUMAN).//Q93074
F-HEMBA1000168//INSULIN RECEPTOR SUBSTRATE-2 (IRS-2) (4PS).//0.00055:86:36//MUS MUSCULUS (MOUSE).//P81122
F-HEMBA1000180//VPU PROTEIN (U ORF PROTEIN).//0.22:73:28//CHIMPANZEE IMMUNODEFICIENCY VIRUS (SIV(CPZ)) (CIV).//P17286
F-HEMBA1000185//RAS-1 PROTEIN.//5.1e-10:121:29//NEUROSPORA CRASSA.//P22126
F-HEMBA1000193//PROLINE-RICH PEPTIDE P-B.//0.00078:56:41//HOMO SAPIENS (HUMAN).//P02814
F-HEMBA1000201//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.00061:49:42//MUS MUSCULUS (MOUSE).//P05142
F-HEMBA1000213
F-HEMBA1000216//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (ARNT INTERACTING PROTEIN).//1.6e-59:115:53//MUS MUSCULUS (MOUSE).//Q61221
F-HEMBA1000227//SUPPRESSOR PROTEIN SRP40.//0.00059:135:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-HEMBA1000231//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I.//0.024:60:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
F-HEMBA1000243//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0038:125:34//HOMO SAPIENS (HUMAN).//P08547
F-HEMBA1000244//HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION.//3.1e-17:149:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40480
F-HEMBA1000251
F-HEMBA1000264//PROBABLE E5 PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVIRUS TYPE 58.//P26552
F-HEMBA1000280//SHORT NEUROTOXIN 1 (TOXIN C-6).//0.98:58:31//NAJA NAJA KAOUTHIA (MONOCLED COBRA) (NAJA NAJA SIAMENSIS).//P14613
F-HEMBA1000282//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.14:26:65//HOMO SAPIENS (HUMAN).//P39188
F-HEMBA1000288
F-HEMBA1000290//HYPOTHETICAL 14 KD PROTEIN IN TVRI-6 REPETITIVE REGION.//3.8e-06:98:39//HOMO SAPIENS (HUMAN).//P10516
F-HEMBA1000302
F-HEMBA1000303//HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN CHROMOSOME III.//1.3e-05:69:42//CAENORHABDITIS ELEGANS.//Q03601
F-HEMBA1000304//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//0.021:18:83//HOMO SAPIENS (HUMAN).//

F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1005077
F-PLACE1005085//INSECT TOXIN 1 (BOT IT1).//0.85:36:33//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753
F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821
F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359
F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGERIN II).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608
F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708
F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075
F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1005176
F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSE PANENCEPHALITIS VIRUS).//P06831
F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.0025:58:34//NEUROSPORA CRASSA.//P38678
F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511
F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218
F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEEANUS.//Q01577
F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN T05H10.7 IN CHROMOSOME II.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003
F-PLACE1005266
F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287
F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352
F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760
F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020
F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:36:41//ESCHERICHIA COLI.//P39355
F-PLACE1005327//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808
F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274
F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067
F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48567
F-PLACE1005374
F-PLACE1005409
F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE).//1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO).//P07979
F-PLACE1005467//KERATIN, FEATHER (F-KER).//0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER

F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III.//4.3e-45:164:48// CAENORHABDITIS ELEGANS.//Q02328
F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0063:99:31//HOMO SAPIENS (HUMAN).//P10161
F-Y79AA1002307
F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III.//0.75:198:24// CAENORHABDITIS ELEGANS.//P46012
F-Y79AA1002351//CUTICLE COLLAGEN 34.//0.74:128:35//CAENORHABDITIS ELEGANS.//P34687
F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2.//0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40036
F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//1.0:89:30//CARASSIUS AURATUS (GOLDFISH).//P17691
F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION.//3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53899
F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE).//6.7e-72:162:84//HOMO SAPIENS (HUMAN).//P17812
F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.81:34:41//HOMO SAPIENS (HUMAN).//P22531
F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68.//0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558
F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35).//2.3e-60:217:44//MUS MUSCULUS (MOUSE).// P15620
F-Y79AA1002482//ZINC FINGER PROTEIN 141.//2.Oe-31:90:55//HOMO SAPIENS (HUMAN).//Q15928
F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I.//0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053

Homology Search Result Data 2. .

[0300] The result of the homology search of the GenBank using the clone sequence of 5'-end except EST and STS.

[0301] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by *//*.

[0302] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953
F-HEMBA1000012//Caenorhabditis-elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787
F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344
F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (GIT1) mRNA, complete cds.//5.6e-124:743:88//AF085693
F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581
F-HEMBA1000046//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 125I3, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528
F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL022477
F-HEMBA1000076//Homo sapiens full-length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182
F-HEMBA1000111//CIT-HSP-2291M18.TF CIT-HSP Homo sapiens genomic clone 2291M18 genomic survey sequence.//2.8e-16:132:79//AQ004134
F-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//8.6e-98:230:93// AC003104
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331
F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60// AF056324
F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741

F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373
F-PLACE1005026
F-PLACE1005027
F-PLACE1005046
F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148
F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569
F-PLACE1005077
F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673
F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316
F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225
F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476
F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081
F-PLACE1005111
F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//L14320
F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=I, genomic survey sequence.//7.4e-38:299:82//AQ103361
F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451
F-PLACE1005176
F-PLACE1005181//CIT-HSP-2340O5.TR CIT-HSP Homo sapiens genomic clone 2340O5, genomic survey sequence.//0.99:211:63//AQ054651
F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445
F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061
F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965
F-PLACE1005243
F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
F-PLACE1005266//H.sapiens mRNA (fetal brain cDNA a4_2g).//9.6e-33:177:98//Z70695
F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
F-PLACE1005308//Clethrionomys glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167
F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794
F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380
F-PLACE1005373
F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104
F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991
F-PLACE1005453//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854
F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859

F-Y79AA1001875//CTT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
F-Y79AA1001923//H.sapiens CpG island DNA genomic Mse1 fragment, clone 193c12, forward read cpg193c12.ft1a.//0.0031:108:75//Z60186
F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526I14, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
F-Y79AA1002089
F-Y79AA1002093//Mus musculus transcription factor like protein 4 TCFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
F-Y79AA1002115
F-Y79AA1002125//H.sapiens (D8S135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
F-Y79AA1002210//Homo sapines chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//6.8e-159:748:98//AB014555
F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
F-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
F-Y79AA1002351//S.clavuligerus pah and cas genes.//1.0:369:58//X84101
F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//4.4e-90:529:88//U49385
F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA, complete cds.//1.0:166:66//U36196
F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
F-Y79AA1002482//Homo sapiens full-length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

Homology Search Result Data 3.

[0303] The result of the homology search of the GenBank using the clone sequence of 3'-end except EST and STS.

[0304] Data include

the name of clone,
definition of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0305] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0306] Data are not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953
R-HEMBA1000030//F.rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864
R-HEMBA1000042//RPCI11-77G23.TV RPCI11 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240
R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696
R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948
R-HEMBA1000076//Homo sapiens clone DJ1021I20, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520
R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684
R-HEMBA1000129//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//2.4e-93:503:93//AC003104
R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340
R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060
R-nnnnnnnnnnnn//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631
R-HEMBA1000158
R-nnnnnnnnnnnn
R-HEMBA1000180//Plasmodium falciparum encoding Pfg27/25.//0.073:292:56//X84904
R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146
R-HEMBA1000193
R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126
R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655
R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548
R-nnnnnnnnnnnn
R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat,.//4.3e-24:400:68//AL009181
R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526
R-HEMBA1000244
R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.//0.16:338:60//L76262
R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012
R-nnnnnnnnnnnn//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037
R-HEMBA1000282//Arabidopsis thaliana BAC IG002P16.//0.71:344:60//AF007270
R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046
R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223
R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105
R-nnnnnnnnnnnn//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131
R-nnnnnnnnnnnn//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802

R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
R-PLACE1004972
R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
R-PLACE1005027
R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-567I1, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
R-PLACE1005077//H.sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495
R-PLACE1005086//RPCI11-30H10.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30H10, genomic survey sequence.//0.13:112:67//B87788
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:232:84//U85195
R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
R-PLACE1005128
R-PLACE1005146
R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
R-nnnnnnnnnnnn//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
R-PLACE1005187//Arabidopsis thaliana chromosome II BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
R-PLACE1005206//Homo sapiens full-length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
R-PLACE1005243
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
R-PLACE1005277//CITBI-E1-2514D4.TF CITBI-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
R-PLACE1005308
R-PLACE1005313//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-103:537:94//AB007960
R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794
R-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380

R-Y79AA1002211//H.sapiens NGAL gene.//1.0:311:59//X99133
R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034557
R-Y79AA1002229
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592
R-Y79AA1002246
R-Y79AAl002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-92:453:97//AB013384
R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534
R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173I12 map 10q25, complete sequence.//1.1e-07:368:61//AC005887
R-Y79AA1002351
R-Y79AA1002361//H.sapiens CpG island DNA genomic Mse1 fragment, clone 65b9, reverse read cpg65b9.rt1a.//0.57:59:79//Z62206
R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//2.0e-98:385:99//AC005920
R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//5.4e-59:490:76//AC004662
R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//6.3e-08:103:80//AC004087
R-Y79AA1002431
R-nnnnnnnnnnn//Mouse transcriptional control element.//0.064:84:71//M17284
R-Y79AA1002472//Homo sapiens chromosome 19, BAC CTY-B-393i15 (BC301323), complete sequence.//1.6e-103:525:96//AC006116
R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//9.7e-38:302:83//AC006238
R-Y79AA1002487//P.falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

Homology Search Result Data 4.

[0307] The result of the homology search of the Human Unigene using the clone sequence of 5'-end.
[0308] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0309] Data are not shown for the clones in which the P-value was higher than 1.

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:AI222069
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157
F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:AI253247
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]//0.00019:192:65//Hs.7900:W22411
F-HEMBA1000050//EST//0.81:74:72//Hs.156298:AI336759
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:AI417910
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:AB018340
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H.sapiens]//5.3e-80:383:98//

F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340
F-PLACE1004814//ESTs, Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284
F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362
F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047
F-PLACE1004827//ESTs//0.78:38:100//Hs.18925:W30943
F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97669
F-PLACE1004838
F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X80910
F-PLACE1004868
F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772
F-PLACE1004900
F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382
F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929
F-PLACE1004918//Human tumor susceptiblity protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130
F-PLACE1004930//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936
F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592
F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851
F-PLACE1004969
F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds//0.031:235:60//Hs.27610:U34605
F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147
F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520
F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831
F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459
F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:H15159
F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943
F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148
F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569
F-PLACE1005077//EST//0.79:283:591/Hs.89276:AA283899
F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740
F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147
F-PLACE1005101//Homo sapiens (clone zapl28) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401
F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561
F-PLACE1005108//Treacher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366
F-PLACE1005111//ESTs//0.66:191.63//Hs.106446:N93227
F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661
F-PLACE1005146//ESTs, Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:H11741
F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087
F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541
F-PLACE1005181//ESTs, Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:AI138605
F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:N70417
F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009
F-PLACE1005232//ESTs, Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370
F-PLACE1005243
F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941

F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-19:142:90//Hs.103349:AI141124
F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332
F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778
F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:AI343173
F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:AI424382
F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611
F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943
F-Y79AAI002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:AI338045
F-Y79AA1002093
F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865
F-Y79AA1002115
F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395
F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955
F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538
F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515
F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotenax]//2.3e-113:568:96//Hs.111637:AA305890
F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984
F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:D42045
F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:AB014592
F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903
F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:AB014555
F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:622:97//Hs.30898:AB014534
F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36069
F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
F-Y79AA1002399
F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
F-Y79AA1002431
F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:AI160765
F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302

Homology Search Result Data 5.

[0310] The result of the homology search of the Human Unigene using the clone sequence of 3'-end.

[0311] Data include

the name of clone,
title of the top hit data,
the P-value: the length of the compared sequence: identity (%), and
the Accession No. of the top hit data, as in the order separated by //.

[0312] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0313] Data are not shown for the clones in which the P-value was higher than 1.

U91985
R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:AI089013
R-nnnnnnnnnnnn//ESTs//5.4e-75:366:97//Hs.48119:AA454227
R-PLACE1005181//EST//0.012:172:66//Hs.147107:AI190589
R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:AI022830
R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:AI197937
R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-104:537:94//Hs.136309:AB007960
R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:AI189343
R-PLACE1005335//ESTs, Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975
R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:344:80//Hs.43681:AL022394
R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1005480//EST//0.99:39:82//Hs.157275:AI364046
R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:AI032875
R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185
R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470
R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:AI291325
R-PLACE1005550//ESTs, Highly similar to HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:458:98//Hs.38114:N62927
R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
R-PLACE1005557//ESTs, Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:AI276023
R-PLACE1005603//ESTs//8.2e-99:533:93//Hs.96357:AI026927
R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
R-PLACE1005630
R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255
R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259

R-nnnnnnnnnnn//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428
R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:AB014592
R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOZYME [D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537
R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534
R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
R-Y79AA1002361
R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000
R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753
R-Y79AA100243//EST//6.6e-23:128:98//Hs.128417:AA975026
R-nnnnnnnnnnn//ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 68 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI207821
R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870
R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788
R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:N66499

Homology Search Result Data 6

[0314] Data obtained by the homology search for full-length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in hit data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of hit data. These items are shown in this order and separated by a double-slash mark, //.

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712
C-HEMBA1000030
C-HEMBA1000046
C-HEMBA1000050
C-HEMBA1000076
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%//P08553
C-HEMBA1000158//HEPATOCYTE NUCLEAR FACTOR 3.-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584
C-HEMBA1000168//CYLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%//P35662
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555
C-HEMBA1000193
C-HEMBA1000227
C-HEMBA1000288
C-HEMBA1000302
C-HEMBA1000304
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91 %//035594
C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//AL049654
C-HEMBA1000387
C-HEMBA1000392

C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE).//4.7E-65//695aa//29%//Q01631
C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170
C-PLACE1004824
C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891
C-PLACE1004885
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//O42643
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDHA).//4.9E-48//198aa//44%//P06151
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds//0//1853bp//98%//AF099936
C-PLACE1004934
C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073
C-PLACE1004982
C-PLACE1005026
C-PLACE1005027
C-PLACE1005046
C-PLACE1005077
C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652
C-PLACE1005111
C-PLACE1005181
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636
C-PLACE1005206
C-PLACE1005232
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577
C-PLACE1005261
C-PLACE1005266
C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760
C-PLACE1005308
C-PLACE1005313
C-PLACE1005327
C-PLACE1005335
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//O33335
C-PLACE1005374
C-PLACE1005480
C-PLACE1005481
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251
C-PLACE1005550
C-PLACE1005554
C-PLACE1005623
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350

AMINYLTRANSFERASE) (GALNAC-T1).//1.70E-84//313aa//48%//Q07537
C-Y79AA1001613//ZINC FINGER PROTEIN 132.//3.80E-91//209aa//41%//P52740
C-Y79AA1001679//Homo sapiens lambda-crystallin mRNA, complete cds.//3.4e-310//1430bp//98%//AF077049
C-Y79AA1001692//Mus musculus strain C57BL/J germ cell-less protein (Gc1) mRNA, complete cds.//1.40E-78//227aa//40%//Q01820
C-Y79AA1001705//Homo sapiens p53 regulated PA26-T2 nuclear protein (PA26) mRNA, complete cds.//3.40E-47//626bp//68%//AF033120
C-Y79AA1001711//Human 60-kdal ribonucleoprotein (Ro) mRNA, complete cds.//1.20E-258//1185bp//99%//J04137
C-Y79AA1001827//Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA, complete cds.//0//1689bp//98%//AF177145
C-Y79AA1001866//Homo sapiens zinc finger protein ZNF180 (ZNF180) mRNA, complete cds.//0//2927bp//97%//AF192913
C-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN).//4.50E-08//135aa//31%//P43489
C-Y79AA1001875//RAS-RELATED PROTEIN RAB-7.//9.40E-12//34aa//97%//P51149
C-Y79AA1001923//Homo sapiens F-box protein Fbx22 (FBX22) gene, partial cds.//7.10E-52//279bp//97%//AF174602
C-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//1.00E-10//94aa//47%//O42643
C-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//9.90E-39//143aa//52%//P42743
C-Y79AA1002083//H.sapiens mRNA for MUF1 protein.//5.00E-163//752bp//99%//X86018
C-Y79AA1002103//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.00E-257//549aa//76%//P16415
C-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1).//9.00E-17//120aa//45%//Q24133
C-Y79AA1002204//COMPLEXIN 2 (SYNAPHIN 1) (921-L).//7.50E-09//131aa//35%//Q13329
C-Y79AA1002208//ANKYRIN.//8.10E-34//188aa//38%//Q02357
C-Y79AA1002209/TYROSYL-TRNA SYNTHETASE (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRRS).//1.60E-72//437aa//39%//P00952
C-Y79AA1002210//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//0.0000018//140aa//25%//Q13829
C-Y79AA1002211//PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN HOMOLOG F40A3.3.//1.70E-17//146aa//35%//O16264
C-Y79AA1002229//DNA CROSS-LINK REPAIR PROTEIN PSO2/SNM1.//7.10E-17//213aa//31%//P30620
C-Y79AA1002246//SYNAPTOTAGMIN V.//1.60E-28//286aa//32%//O00445
C-Y79AA1002258//Homo sapiens mRNA for HIP1R, complete cds.//0//2106bp//99%//AB013384
C-Y79AA1002307//Homo sapiens astrotactin2 (ASTN2) mRNA, complete cds.//0//1209bp//99%//AF116574
C-Y79AA1002311//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.90E-186//1130bp//82%//X67877
C-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//6.90E-140//966bp//82%//Y18208
C-Y79AA1002399//Homo sapiens mRNA for sperm protein.//0//1163bp//95%//X91879
C-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsH) mRNA, complete cds.//3.9e-317//1902bp//86%//U49385
C-Y79AA1002431//TRANSDUCIN-LIKE ENHANCER PROTEIN 2 (ESG2).//9.80E-62//318aa//35%//Q04725
C-Y79AA1002433//Homo sapiens chromatin- specific transcription elongation factor FACT 140 kDa subunit mRNA, complete cds.//0//1545bp//96%//AF152961
C-Y79AA1002472//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.50E-136//472aa//49%//Q05481
C-Y79AA1002482//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//2.70E-137//340aa//51%//Q05481
C-Y79AA1002487//Homo sapiens chromosome 5 F-box protein Fbx4 (FBX4) mRNA, complete cds.//7.3e-311//1444bp//98%//AF129534

Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set

forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, or the complementary strand thereof, wherein said oligonucleotide is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucleotides.

2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth in any one of SEQ ID NOs: 1-5547 and SEQ ID NOs: 16111-16164, wherein said oligonucleotide comprises at least 15 nucleotides.

3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide comprising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence 3'-end nucleotide sequence is selected from the group consisting of:

SEQ ID NO: 1 / SEQ ID NO: 5548, SEQ ID NO: 4 / SEQ ID NO: 5549, SEQ ID NO: 5 / SEQ ID NO: 5550, SEQ ID NO: 6 / SEQ ID NO: 5551, SEQ ID NO: 7 / SEQ ID NO: 5552, SEQ ID NO: 8 / SEQ ID NO: 5553, SEQ ID NO: 9 / SEQ ID NO: 5554, SEQ ID NO: 10 / SEQ ID NO: 5555, SEQ ID NO: 11 / SEQ ID NO: 5556, SEQ ID NO: 12 / SEQ ID NO: 5557, SEQ ID NO: 13 / SEQ ID NO: 5558, SEQ ID NO: 14 / SEQ ID NO: 5559, SEQ ID NO: 15 / SEQ ID NO: 5560, SEQ ID NO: 16 / SEQ ID NO: 5561, SEQ ID NO: 17 / SEQ ID NO: 5562, SEQ ID NO: 18 / SEQ ID NO: 5563, SEQ ID NO: 19 / SEQ ID NO: 5564, SEQ ID NO: 20 / SEQ ID NO: 5565, SEQ ID NO: 21 / SEQ ID NO: 5566, SEQ ID NO: 22 / SEQ ID NO: 5567, SEQ ID NO: 23 / SEQ ID NO: 5568, SEQ ID NO: 24 / SEQ ID NO: 5569, SEQ ID NO: 25 / SEQ ID NO: 5570, SEQ ID NO: 26 / SEQ ID NO: 5571, SEQ ID NO: 27 / SEQ ID NO: 5572, SEQ ID NO: 28 / SEQ ID NO: 5573, SEQ ID NO: 29 / SEQ ID NO: 5574, SEQ ID NO: 30 / SEQ ID NO: 5575, SEQ ID NO: 31 / SEQ ID NO: 5576, SEQ ID NO: 32 / SEQ ID NO: 5577, SEQ ID NO: 33 / SEQ ID NO: 5578, SEQ ID NO: 34 / SEQ ID NO: 5579, SEQ ID NO: 35 / SEQ ID NO: 5580, SEQ ID NO: 37 / SEQ ID NO: 5581, SEQ ID NO: 38 / SEQ ID NO: 5582, SEQ ID NO: 39 / SEQ ID NO: 5583, SEQ ID NO: 40 / SEQ ID NO: 5584, SEQ ID NO: 42 / SEQ ID NO: 5585, SEQ ID NO: 43 / SEQ ID NO: 5586, SEQ ID NO: 44 / SEQ ID NO: 5587, SEQ ID NO: 45 / SEQ ID NO: 5588, SEQ ID NO: 46 / SEQ ID NO: 5589, SEQ ID NO: 47 / SEQ ID NO: 5590, SEQ ID NO: 48 / SEQ ID NO: 5591, SEQ ID NO: 49 / SEQ ID NO: 5592, SEQ ID NO: 50 / SEQ ID NO: 5593, SEQ ID NO: 51 / SEQ ID NO: 5594, SEQ ID NO: 52 / SEQ ID NO: 5595, SEQ ID NO: 53 / SEQ ID NO: 5596, SEQ ID NO: 54 / SEQ ID NO: 5597, SEQ ID NO: 55 / SEQ ID NO: 5598, SEQ ID NO: 56 / SEQ ID NO: 5599, SEQ ID NO: 57 / SEQ ID NO: 5600, SEQ ID NO: 58 / SEQ ID NO: 5601, SEQ ID NO: 59 / SEQ ID NO: 5602, SEQ ID NO: 60 / SEQ ID NO: 5603, SEQ ID NO: 61 / SEQ ID NO: 5604, SEQ ID NO: 62 / SEQ ID NO: 5605, SEQ ID NO: 63 / SEQ ID NO: 5606, SEQ ID NO: 65 / SEQ ID NO: 5607, SEQ ID NO: 66 / SEQ ID NO: 5608, SEQ ID NO: 67 / SEQ ID NO: 5609, SEQ ID NO: 68 / SEQ ID NO: 5610, SEQ ID NO: 69 / SEQ ID NO: 5611, SEQ ID NO: 70 / SEQ ID NO: 5612, SEQ ID NO: 71 / SEQ ID NO: 5613, SEQ ID NO: 72 / SEQ ID NO: 5614, SEQ ID NO: 74 / SEQ ID NO: 5615, SEQ ID NO: 76 / SEQ ID NO: 5616, SEQ ID NO: 77 / SEQ ID NO: 5617, SEQ ID NO: 78 / SEQ ID NO: 5618, SEQ ID NO: 79 / SEQ ID NO: 5619, SEQ ID NO: 80 / SEQ ID NO: 5620, SEQ ID NO: 81 / SEQ ID NO: 5621, SEQ ID NO: 82 / SEQ ID NO: 5622, SEQ ID NO: 83 / SEQ ID NO: 5623, SEQ ID NO: 84 / SEQ ID NO: 5624, SEQ ID NO: 85 / SEQ ID NO: 5625, SEQ ID NO: 86 / SEQ ID NO: 5626, SEQ ID NO: 87 / SEQ ID NO: 5627, SEQ ID NO: 88 / SEQ ID NO: 5628, SEQ ID NO: 89 / SEQ ID NO: 5629, SEQ ID NO: 90 / SEQ ID NO: 5630, SEQ ID NO: 91 / SEQ ID NO: 5631, SEQ ID NO: 92 / SEQ ID NO: 5632, SEQ ID NO:

93 / SEQ ID NO: 5633, SEQ ID NO: 94 / SEQ ID NO: 5634, SEQ ID NO: 95 / SEQ ID NO: 5635, SEQ ID NO: 96 / SEQ ID NO: 5636, SEQ ID NO: 97 / SEQ ID NO: 5637, SEQ ID NO: 98 / SEQ ID NO: 5638, SEQ ID NO: 99 / SEQ ID NO: 5639, SEQ ID NO: 100 / SEQ ID NO: 5640, SEQ ID NO: 101 / SEQ ID NO: 5641, SEQ ID NO: 102 / SEQ ID NO: 5642, SEQ ID NO: 103 / SEQ ID NO: 5643, SEQ ID NO: 104 / SEQ ID NO: 5644, SEQ ID NO: 105 / SEQ ID NO: 5645, SEQ ID NO: 106 / SEQ ID NO: 5646, SEQ ID NO: 107 / SEQ ID NO: 5647, SEQ ID NO: 108 / SEQ ID NO: 5648, SEQ ID NO: 109 / SEQ ID NO: 5649, SEQ ID NO: 110 / SEQ ID NO: 5650, SEQ ID NO: 111 / SEQ ID NO: 5651, SEQ ID NO: 112 / SEQ ID NO: 5652, SEQ ID NO: 113 / SEQ ID NO: 5653, SEQ ID NO: 114 / SEQ ID NO: 5654, SEQ ID NO: 115 / SEQ ID NO: 5655, SEQ ID NO: 116 / SEQ ID NO: 5656, SEQ ID NO: 117 / SEQ ID NO: 5657, SEQ ID NO: 118 / SEQ ID NO: 5658, SEQ ID NO: 119 / SEQ ID NO: 5659, SEQ ID NO: 120 / SEQ ID NO: 5660, SEQ ID NO: 121 / SEQ ID NO: 5661, SEQ ID NO: 122 / SEQ ID NO: 5662, SEQ ID NO: 123 / SEQ ID NO: 5663, SEQ ID NO: 124 / SEQ ID NO: 5664, SEQ ID NO: 125 / SEQ ID NO: 5665, SEQ ID NO: 126 / SEQ ID NO: 5666, SEQ ID NO: 127 / SEQ ID NO: 5667, SEQ ID NO: 128 / SEQ ID NO: 5668, SEQ ID NO: 129 / SEQ ID NO: 5669, SEQ ID NO: 130 / SEQ ID NO: 5670, SEQ ID NO: 131 / SEQ ID NO: 5671, SEQ ID NO: 132 / SEQ ID NO: 5672, SEQ ID NO: 133 / SEQ ID NO: 5673, SEQ ID NO: 134 / SEQ ID NO: 5674, SEQ ID NO: 135 / SEQ ID NO: 5675, SEQ ID NO: 136 / SEQ ID NO: 5676, SEQ ID NO: 137 / SEQ ID NO: 5677, SEQ ID NO: 138 / SEQ ID NO: 5678, SEQ ID NO: 139 / SEQ ID NO: 5679, SEQ ID NO: 140 / SEQ ID NO: 5680, SEQ ID NO: 141 / SEQ ID NO: 5681, SEQ ID NO: 142 / SEQ ID NO: 5682, SEQ ID NO: 143 / SEQ ID NO: 5683, SEQ ID NO: 144 / SEQ ID NO: 5684, SEQ ID NO: 145 / SEQ ID NO: 5685, SEQ ID NO: 146 / SEQ ID NO: 5686, SEQ ID NO: 147 / SEQ ID NO: 5687, SEQ ID NO: 148 / SEQ ID NO: 5688, SEQ ID NO: 149 / SEQ ID NO: 5689, SEQ ID NO: 150 / SEQ ID NO: 5690, SEQ ID NO: 151 / SEQ ID NO: 5691, SEQ ID NO: 153 / SEQ ID NO: 5692, SEQ ID NO: 154 / SEQ ID NO: 5693, SEQ ID NO: 155 / SEQ ID NO: 5694, SEQ ID NO: 156 / SEQ ID NO: 5695, SEQ ID NO: 157 / SEQ ID NO: 5696, SEQ ID NO: 158 / SEQ ID NO: 5697, SEQ ID NO: 159 / SEQ ID NO: 5698, SEQ ID NO: 160 / SEQ ID NO: 5699, SEQ ID NO: 161 / SEQ ID NO: 5700, SEQ ID NO: 162 / SEQ ID NO: 5701, SEQ ID NO: 163 / SEQ ID NO: 5702, SEQ ID NO: 164 / SEQ ID NO: 5703, SEQ ID NO: 165 / SEQ ID NO: 5704, SEQ ID NO: 166 / SEQ ID NO: 5705, SEQ ID NO: 167 / SEQ ID NO: 5706, SEQ ID NO: 168 / SEQ ID NO: 5707, SEQ ID NO: 169 / SEQ ID NO: 5708, SEQ ID NO: 170 / SEQ ID NO: 5709, SEQ ID NO: 171 / SEQ ID NO: 5710, SEQ ID NO: 173 / SEQ ID NO: 5711, SEQ ID NO: 174 / SEQ ID NO: 5712, SEQ ID NO: 175 / SEQ ID NO: 5713, SEQ ID NO: 176 / SEQ ID NO: 5714, SEQ ID NO: 177 / SEQ ID NO: 5715, SEQ ID NO: 178 / SEQ ID NO: 5716, SEQ ID NO: 179 / SEQ ID NO: 5717, SEQ ID NO: 180 / SEQ ID NO: 5718, SEQ ID NO: 181 / SEQ ID NO: 5719, SEQ ID NO: 182 / SEQ ID NO: 5720, SEQ ID NO: 183 / SEQ ID NO: 5721, SEQ ID NO: 184 / SEQ ID NO: 5722, SEQ ID NO: 185 / SEQ ID NO: 5723, SEQ ID NO: 186 / SEQ ID NO: 5724, SEQ ID NO: 187 / SEQ ID NO: 5725, SEQ ID NO: 188 / SEQ ID NO: 5726, SEQ ID NO: 189 / SEQ ID NO: 5727, SEQ ID NO: 190 / SEQ ID NO: 5728, SEQ ID NO: 191 / SEQ ID NO: 5729, SEQ ID NO: 192 / SEQ ID NO: 5730, SEQ ID NO: 193 / SEQ ID NO: 5731, SEQ ID NO: 194 / SEQ ID NO: 5732, SEQ ID NO: 195 / SEQ ID NO: 5733, SEQ ID NO: 196 / SEQ ID NO: 5734, SEQ ID NO: 197 / SEQ ID NO: 5735, SEQ ID NO: 198 / SEQ ID NO: 5736, SEQ ID NO: 199 / SEQ ID NO: 5737, SEQ ID NO: 200 / SEQ ID NO: 5738, SEQ ID NO: 201 / SEQ ID NO: 5739, SEQ ID NO: 202 / SEQ ID NO: 5740, SEQ ID NO: 203 / SEQ ID NO: 5741, SEQ ID NO: 204 / SEQ ID NO: 5742, SEQ ID NO: 205 / SEQ ID NO: 5743, SEQ ID NO: 206 / SEQ ID NO: 5744, SEQ ID NO: 207 / SEQ ID NO: 5745, SEQ ID NO: 208 / SEQ ID NO: 5746, SEQ ID NO: 209 / SEQ ID NO: 5747, SEQ ID NO: 210 / SEQ ID NO: 5748, SEQ ID NO: 211 / SEQ ID NO: 5749, SEQ ID NO: 212 / SEQ ID NO: 5750, SEQ ID NO: 213 / SEQ ID NO: 5751, SEQ ID NO: 214 / SEQ ID NO: 5752, SEQ ID NO: 215 / SEQ ID NO: 5753, SEQ ID NO: 216 / SEQ ID NO: 5754, SEQ ID NO: 217 / SEQ ID NO: 5755, SEQ ID NO: 218 / SEQ ID NO: 5756, SEQ ID NO: 219 / SEQ ID NO: 5757, SEQ ID NO: 220 / SEQ ID NO: 5758, SEQ ID NO: 221 / SEQ ID NO: 5759, SEQ ID NO: 222 / SEQ ID NO: 5760, SEQ ID NO: 223 / SEQ ID NO: 5761, SEQ ID NO: 224 / SEQ ID NO: 5762,

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NO: 16216, SEQ ID NO: 16163 / SEQ ID NO: 16217, and SEQ ID NO: 16164 / SEQ ID NO: 16218

4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.

5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.

6. A substantially pure protein encoded by polynucleotide of claim 4.

7. A partial peptide of the protein of claim 6.

8. An isolated polynucleotide selected from the group consisting of

(a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

SEQ ID NO: 10468, SEQ ID NO: 10470, SEQ ID NO: 10471, SEQ ID NO: 10472, SEQ ID NO: 10473, SEQ ID NO: 10475, SEQ ID NO: 10477, SEQ ID NO: 10479, SEQ ID NO: 10481, SEQ ID NO: 10483, SEQ ID NO: 10485, SEQ ID NO: 10487, SEQ ID NO: 10488, SEQ ID NO: 10489, SEQ ID NO: 10491, SEQ ID NO: 10493, SEQ ID NO: 10495, SEQ ID NO: 10496, SEQ ID NO: 10497, SEQ ID NO: 10498, SEQ ID NO: 10500, SEQ ID NO: 10502, SEQ ID NO: 10503, SEQ ID NO: 10504, SEQ ID NO: 10505, SEQ ID NO: 10507, SEQ ID NO: 10508, SEQ ID NO: 10510, SEQ ID NO: 10511, SEQ ID NO: 10512, SEQ ID NO: 10514, SEQ ID NO: 10516, SEQ ID NO: 10517, SEQ ID NO: 10519, SEQ ID NO: 10521, SEQ ID NO: 10523, SEQ ID NO: 10524, SEQ ID NO: 10526, SEQ ID NO: 10528, SEQ ID NO: 10529, SEQ ID NO: 10530, SEQ ID NO: 10532, SEQ ID NO: 10534, SEQ ID NO: 10535, SEQ ID NO: 10537, SEQ ID NO: 10539, SEQ ID NO: 10540, SEQ ID NO: 10542, SEQ ID NO: 10543, SEQ ID NO: 10545, SEQ ID NO: 10546, SEQ ID NO: 10548, SEQ ID NO: 10550, SEQ ID NO: 10551, SEQ ID NO: 10553, SEQ ID NO: 10555, SEQ ID NO: 10556, SEQ ID NO: 10557, SEQ ID NO: 10558, SEQ ID NO: 10560, SEQ ID NO: 10562, SEQ ID NO: 10564, SEQ ID NO: 10566, SEQ ID NO: 10567, SEQ ID NO: 10569, SEQ ID NO: 10571, SEQ ID NO: 10573, SEQ ID NO: 10574, SEQ ID NO: 10576, SEQ ID NO: 10578, SEQ ID NO: 10580, SEQ ID NO: 10582, SEQ ID NO: 10584, SEQ ID NO: 10586, SEQ ID NO: 10588, SEQ ID NO: 10590, SEQ ID NO: 10592, SEQ ID NO: 10594, SEQ ID NO: 10596, SEQ ID NO: 10597, SEQ ID NO: 10599, SEQ ID NO: 10601, SEQ ID NO: 10603, SEQ ID NO: 10604, SEQ ID NO: 10606, SEQ ID NO: 10607, SEQ ID NO: 10609, SEQ ID NO: 10611, SEQ ID NO: 10613, SEQ ID NO: 10614, SEQ ID NO: 10615, SEQ ID NO: 10616, SEQ ID NO: 10618, SEQ ID NO: 10619, SEQ ID NO: 10620, SEQ ID NO: 10622, SEQ ID NO: 10624, SEQ ID NO: 10625, SEQ ID NO: 10627, SEQ ID NO: 10629,

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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence set forth in any one of the following SEQ ID NOs:

SEQ ID NO:10469, SEQ ID NO:10474, SEQ ID NO:10476, SEQ ID NO:10478, SEQ ID NO:10480, SEQ ID NO:10482, SEQ ID NO:10484, SEQ ID NO:10486, SEQ ID NO:10490, SEQ ID NO:10492, SEQ ID NO:10494, SEQ ID NO:10499, SEQ ID NO:10501, SEQ ID NO:10506, SEQ ID NO:10509, SEQ ID NO:10513, SEQ ID NO:10515, SEQ ID NO:10518, SEQ ID NO:10520, SEQ ID NO:10522, SEQ ID NO:10525, SEQ ID NO:10527, SEQ ID NO:10531, SEQ ID NO:10533, SEQ ID NO:10536, SEQ ID NO:10538, SEQ ID NO:10541, SEQ ID NO:10544, SEQ ID NO:10547, SEQ ID NO:10549, SEQ ID NO:10552, SEQ ID NO:10554, SEQ ID NO:10559, SEQ ID NO:10561, SEQ ID NO:10563, SEQ ID NO:10565, SEQ ID NO:10568, SEQ ID NO:10570, SEQ ID NO:10572, SEQ ID NO:10575, SEQ ID NO:10577, SEQ ID NO:10579, SEQ ID NO:10581, SEQ ID NO:10583, SEQ ID NO:10585, SEQ ID NO:10587, SEQ ID NO:10589, SEQ ID NO:10591, SEQ ID NO:10593, SEQ ID NO:10595, SEQ ID NO:10598, SEQ ID NO:10600, SEQ ID NO:10602, SEQ ID NO:10605, SEQ ID NO:10608, SEQ ID NO:10610, SEQ ID NO:10612, SEQ ID NO:10617, SEQ ID NO:10621, SEQ ID NO:10623, SEQ ID NO:10626, SEQ ID NO:10628, SEQ ID NO:10631, SEQ ID NO:10634, SEQ ID NO:10636, SEQ ID NO:10638, SEQ ID NO:10640, SEQ ID NO:10643, SEQ ID NO:10645, SEQ ID NO:10651, SEQ ID NO:10653, SEQ ID NO:10657, SEQ ID NO:10660, SEQ ID NO:10662, SEQ ID NO:10664, SEQ ID NO:10666, SEQ ID NO:10668, SEQ ID NO:10672, SEQ ID NO:10675, SEQ ID NO:10677, SEQ ID NO:10679, SEQ ID NO:10681, SEQ ID NO:10684, SEQ ID NO:10686, SEQ ID NO:10688, SEQ ID NO:10690, SEQ ID NO:10692, SEQ ID NO:10694, SEQ ID NO:10697, SEQ ID NO:10699, SEQ ID NO:10701, SEQ ID NO:10703, SEQ ID NO:10705, SEQ ID NO:10707, SEQ ID NO:10709, SEQ ID NO:10712, SEQ ID NO:10714, SEQ ID NO:10716, SEQ ID NO:10719, SEQ ID NO:10721,

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(c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
(d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
(e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
(f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).

9. A substantially pure protein encoded by the polynucleotide of claim 8.

10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.

11. A vector comprising the polynucleotide of claim 5 or 8.

12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.

14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.

15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.

16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.

17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.

18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.

19. A method for synthesizing a polynucleotide, the method comprising:

a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
b) recovering the synthesized product.

20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.

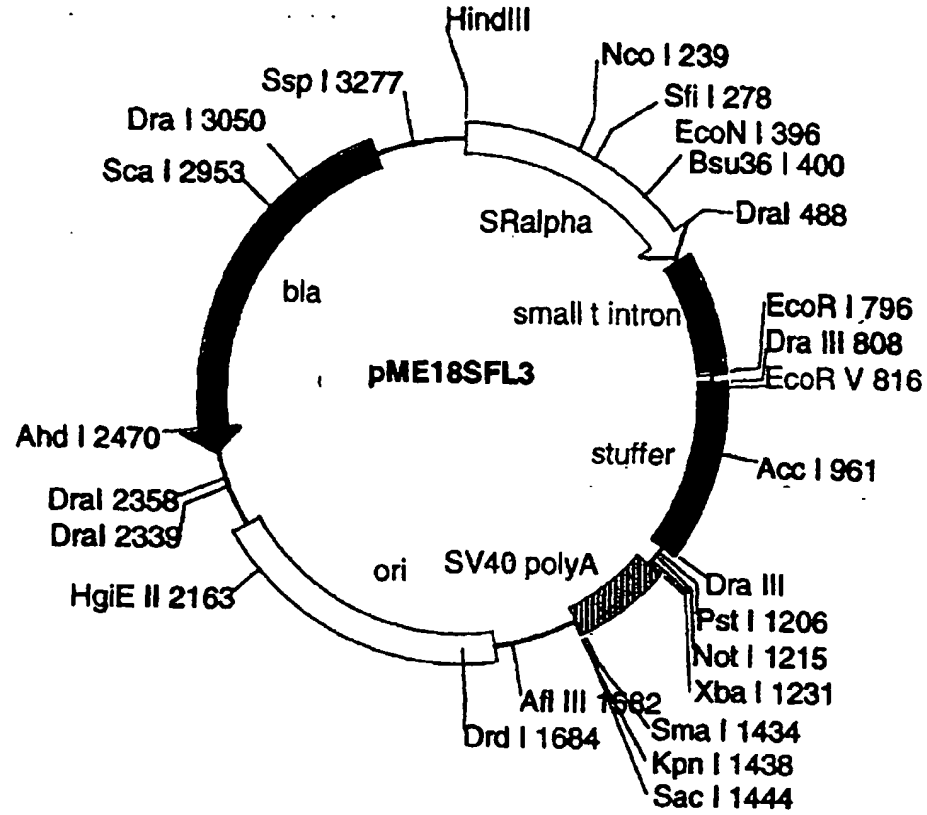
21. The method of claim 19, wherein the complementary strand is obtainable by PCR.

22. A method for detecting the polynucleotide of claim 8, the method comprising:

a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.

23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium on which the database is stored.

Figure 1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Ssp I 3277
Sfi I 278
Dra I 3050
EcoN I 396
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Bsu36 I 400
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bla
small t intron
EcoR I 796
Dra III 808
pME18SFL3
EcoR V 816
Ahd I 2470
stuffer
Acc I 961
DraI 2358
DraI 2339
ori
SV40 polyA
Dra III
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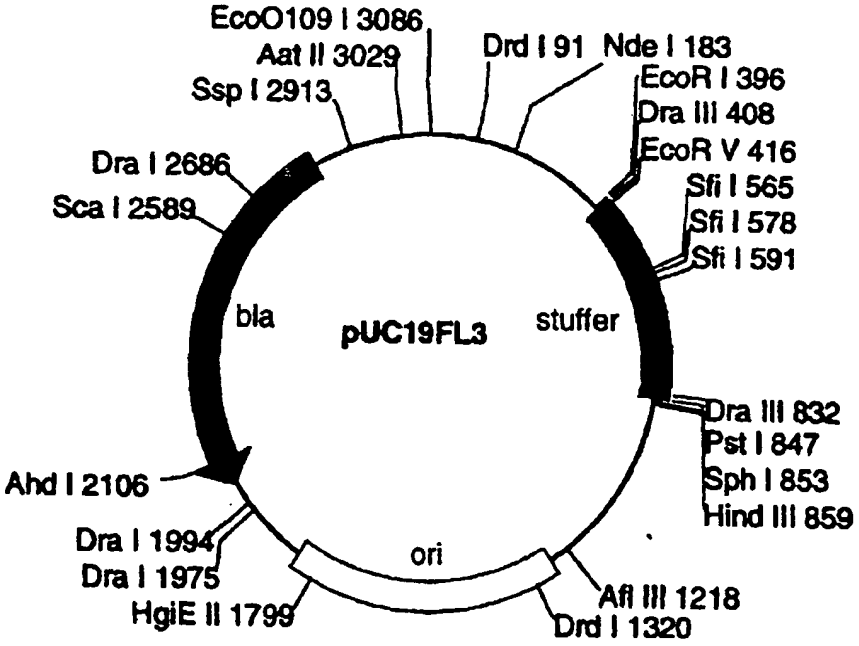
Sac I 1444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Sfi I 565
Sfi I 578
Sfi I 591
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stuffer
Dra III 832
Pst I 847
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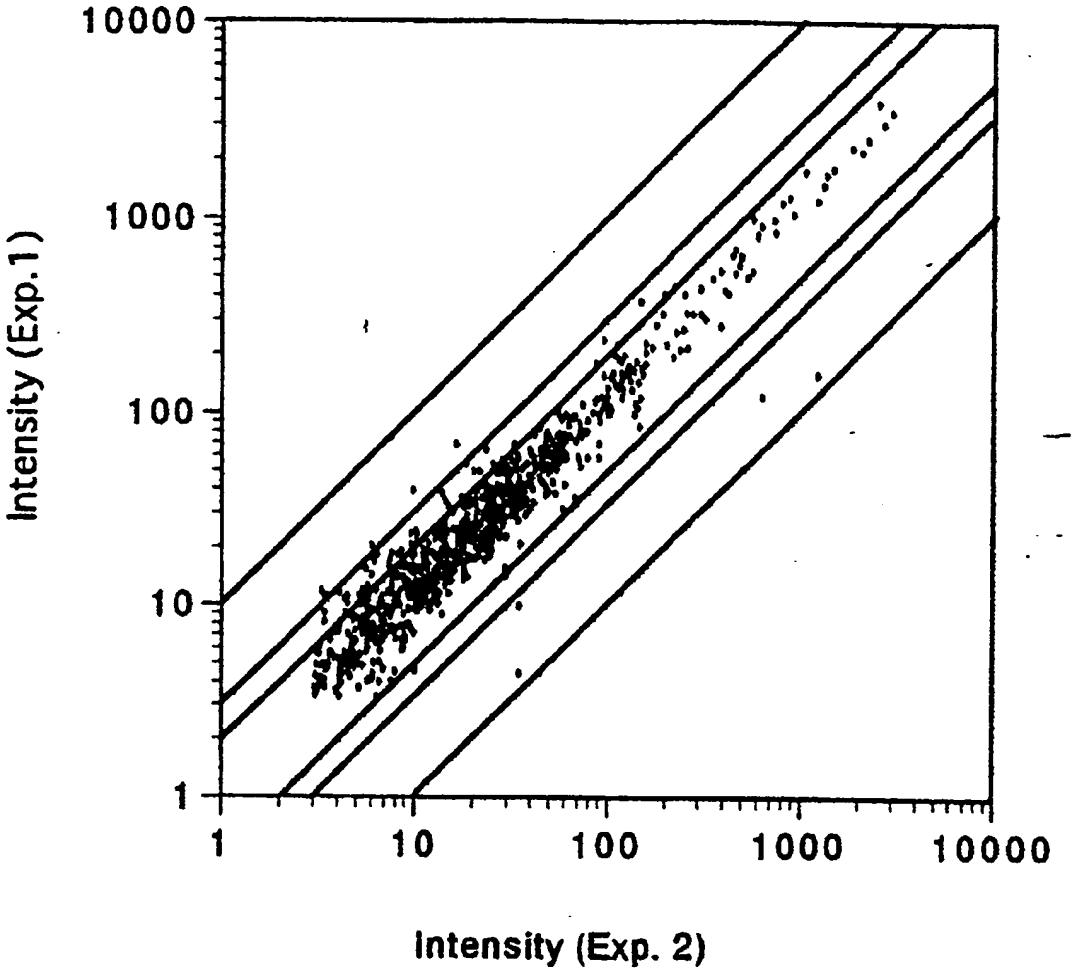
Figure 2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Intensity (Exp. 2)

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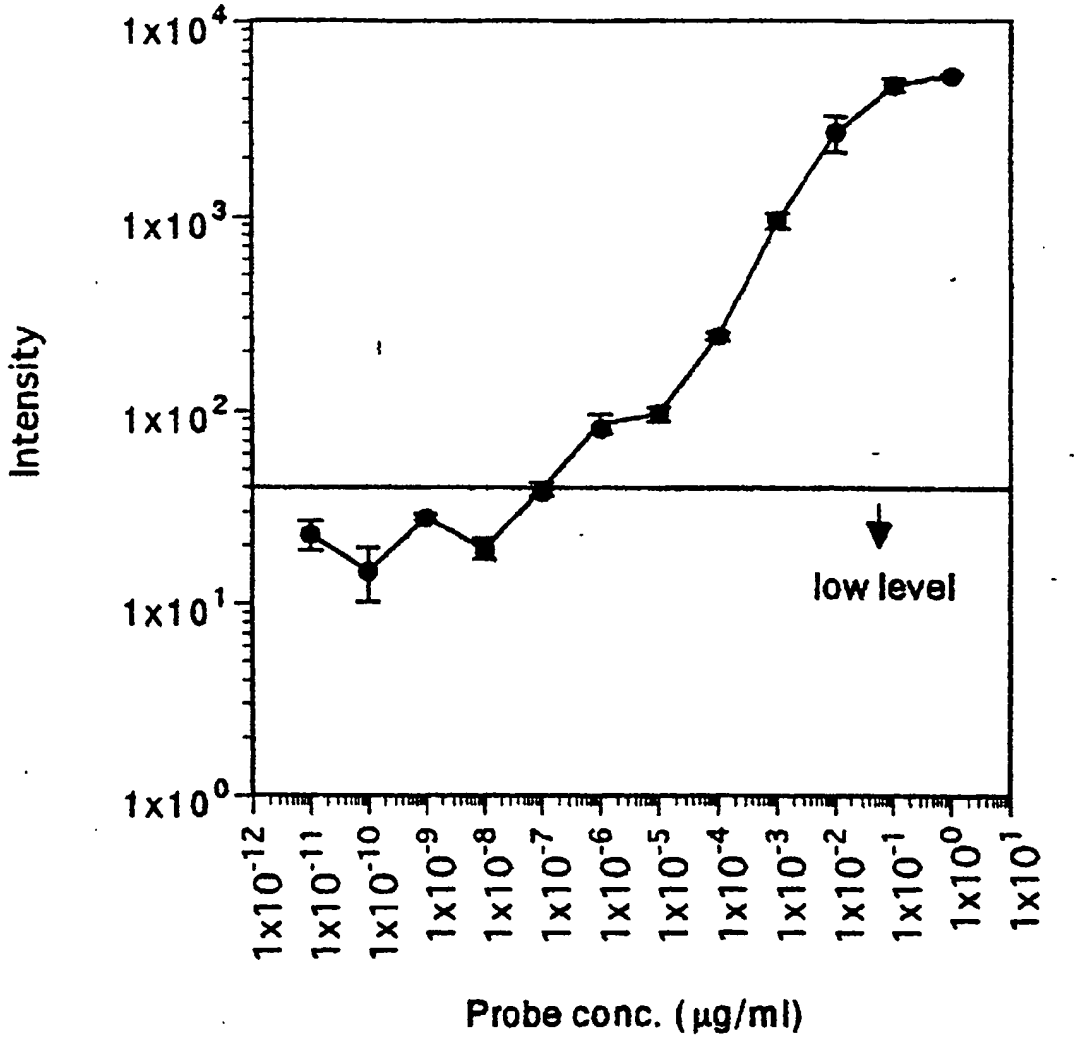
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1x10^-6
1x10^-5
1x10^-4
1x10^-3
1x10^-2
1x10^-1
1x10^0
1x10^1
Probe conc. (µg/ml)

(19) Europäisches Patentamt
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(54) Primers for synthesising full-length cDNA and their use

(57) Primers for synthesizing full-length cDNAs and their use are provided.

5602 cDNA encoding a human protein has been isolated and nucleotide sequences of 5'-, and 3' -ends of the cDNA have been determined. Furthermore, primers for synthesizing the full-length cDNA have been provided to clarify the function of the protein encoded by the cDNA. The full-length cDNA of the present invention containing the translation start site provides information useful for analyzing the functions of the protein.

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European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

which under Rule 45 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

Application Number EP 00 11 6126

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
X	BRIGHTMAN S E ET AL: "Isolation of a mouse cDNA encoding MTJ1, a new murine member of the DnaJ family of proteins" GENE, ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, NL, vol. 153, no. 2, 14 February 1995 (1995-02-14), pages 249-254, XP004042536 ISSN: 0378-1119 * abstract; figures 1,3,5 *	1-22	C12N15/12 C12N15/11 C07K14/47 C07K16/18 C12Q1/68
X	DATABASE EMBL [Online] 23 November 1998 (1998-11-23), STRAUSBERG: "ql71b04.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1877743 3 similar to SW:MTJ1_MOUSE Q61712 DNAJ PROTEIN HOMOLOG MTJ1. ;, mRNA" XP002270645 accession no. EBI Database accession no. AI276458 * the whole document *	1-22	
	-/--		TECHNICAL FIELDS SEARCHED (Int.Cl.7) C07K C12N

INCOMPLETE SEARCH

The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.

Claims searched completely :

Claims searched incompletely :

Claims not searched :

Reason for the limitation of the search:

see sheet C

Place of search	Date of completion of the search	Examiner
The Hague	18 February 2004	Gurdjian, D

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C07)

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INCOMPLETE SEARCH
SHEET C

Application Number
EP 00 11 6126

Claim(s) not searched:
23

Reason for the limitation of the search (non-patentable invention(s)):

Article 52 (2)(d) EPC - Presentation of information

European Patent Office

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Application Number
EP 00 11 6126

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	
X	DATABASE EMBL [Online] 31 December 1998 (1998-12-31), STRAUSBERG: "tb98c06.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062378 3' similar to SW:MTJ1_MOUSE Q61712 DNAJ PROTEIN HOMOLOG MTJ1. ;, mRNA sequence." XP002270646 accession no. EBI Database accession no. AI337322 * the whole document * -----	1-22	
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EPO FORM 1503 03.82 (P04C10)

European Patent Office

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 00 11 6126

DOCUMENTS CONSIDERED TO BE RELEVANT			CLASSIFICATION OF THE APPLICATION (Int.Cl.7)
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P,X	DATABASE EMBL [Online] 22 February 2000 (2000-02-22), ISOGAI T.: "Homo sapiens cDNA FLJ10199 fis, clone HEMBA1004850." XP002270649 accession no. EBI Database accession no. AK001061 * the whole document * -----	1-22	TECHNICAL FIELDS SEARCHED (Int.Cl.7)
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EPO FORM 1503 03.82 (P04C10)

European Patent Office

Application Number
EP 00 11 6126

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet B

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☒ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

1-22

☐ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:

European Patent Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 00 11 6126

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

1. claims: 1-23 partly

Invention 1 :

A primer set for synthesizing polynucleotides, the primer set comprising oligonucleotide complementary to the complementary strand of the polynucleotide comprising the nucleotide sequences set forth in of SEQ ID NO:1,5548 where seq.1 is corresponding to the 5'end of polynucleotide of clone HEMBA1000005 having seq.id.10468 ,corresponding coding region in the polynucleotide with corresponding protein with amino acid sequence with seq.id.10469 , and method for synthesizing a polynucleotide.

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2. claims: 1-23 partly

Inventions 2-5602 :

A primer set for synthesizing polynucleotides, the primer set comprising oligonucleotide complementary to the complementary strand of the polynucleotide probably corresponding to the 5'end and 3' end of polynucleotide of the 5601 clones as disclosed on tables 1 and 2 of the present application , or as disclosed on pages 127 line 33-page 130 line 47 combined with example 11 of the present application , the polynucleotide of this clone, coresponding coding region in the polynucleotide with corresponding protein , and method for synthesizing a polynucleotide.

ANNEX TO THE EUROPEAN SEARCH REPORT ON EUROPEAN PATENT APPLICATION NO. EP 00 11 6126

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

18-02-2004

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82